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# OM protein - protein search, using SW model

Run on: December 2, 2004, 22:07:09 / Search time 162 Seconds  
(without alignments)  
1643.069 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858  
Sequence: 1 MADSSBGPAPGAEVAAELPG.....GQVSKSKHIMKLGRRRL 742

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_23Sep04:\*

- 1: geneeqp1980s:\*
- 2: geneeqp1990s:\*
- 3: geneeqp2000s:\*
- 4: geneeqp2001s:\*
- 5: geneeqp2002s:\*
- 6: geneeqp2003as:\*
- 7: geneeqp2003bs:\*
- 8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	4	AAE06683 Human van
2	3829	99.2	831	8	AD181606 Human van
3	3829	99.2	871	4	AAE01227 Human van
4	3829	99.2	871	4	AAE01227 Human van
5	3829	99.2	871	5	AAE01227 Human van
6	3829	99.2	871	5	AAE01227 Human van
7	3829	99.2	871	5	AAE01227 Human van
8	3829	99.2	871	5	AAE01227 Human van
9	3829	99.2	871	5	AAE01227 Human van
10	3829	99.2	871	5	AAE01227 Human van
11	3829	99.2	871	5	AAE01227 Human van
12	3829	99.2	871	5	AAE01227 Human van
13	3829	99.2	871	5	AAE01227 Human van
14	3829	99.2	871	5	AAE01227 Human van
15	3829	99.2	871	5	AAE01227 Human van
16	3829	99.2	871	5	AAE01227 Human van
17	3829	99.2	871	5	AAE01227 Human van
18	3829	99.2	871	5	AAE01227 Human van
19	3829	99.2	871	5	AAE01227 Human van
20	3829	99.2	871	5	AAE01227 Human van
21	3829	99.2	871	5	AAE01227 Human van
22	3829	99.2	871	5	AAE01227 Human van
23	3829	99.2	871	5	AAE01227 Human van
24	3829	99.2	871	5	AAE01227 Human van
25	3829	99.2	871	5	AAE01227 Human van

26	3689	95.6	871	8	AD181610 Mouse OTR
27	3685	95.5	871	7	AD332559 Murine TR
28	3681	95.4	871	4	AAE07209 Amino aci
29	3636	94.2	873	8	AD181594 Mouse van
30	3472	90.0	803	8	AD181586 Human van
31	3470	89.9	811	4	AAE06682 Human van
32	3467	89.9	803	4	AAE06208 Amino aci
33	3389	87.8	803	8	AD181592 Mouse van
34	3284	85.1	852	8	AD181566 Chicken v
35	3120	80.9	743	4	AAE03209 Amino aci
36	2373.5	61.5	602	5	AAU74936 Amino aci
37	2315.5	60.0	1115	4	ABG28242 Novel hum
38	2156.5	55.9	559	5	AAE16773 Human tra
39	1808	46.9	498	4	AAE04889 Human tra
40	1604.5	41.6	843	2	AAE06561 Chicken v
41	1601.5	41.5	843	2	AAW99799 Chicken v
42	1580.5	41.0	838	8	AD181568 Rat vanil
43	1579.5	40.9	838	2	AAE06555 Rat capsa
44	1579.5	40.9	838	2	AAW99789 Rat VRL C
45	1579.5	40.9	838	4	AAE01228 Rattus va

## ALIGNMENTS

RESULT 1  
AAE06683  
ID AAE06683 standard; protein; 742 AA.  
XX  
AC AAE06683;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human vanilloid receptor VR3 isoform, VR3A+B+.  
KW Human; vanilloid receptor; VR3; inflammatory condition; analgesic;  
KW intracable pain; postherpetic neuralgia; diabetic neuropathy; asthma;  
KW postmastectomy pain; complex regional pain syndrome; arthritis;  
KW rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;  
KW chronic obstructive pulmonary disease; irritable bowel syndrome;  
KW psoriasis; central nervous system disease; CNS; cancer;  
KW intestinal tract disorder; VR3A+B+.  
XX  
OS Homo sapiens.  
XX  
PN WO200158945-A1.  
XX  
PD 16-AUG-2001.  
XX  
PF 01-FEB-2001; 2001WO-US003456.  
XX  
PR 08-FEB-2000; 2000US-00500123.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Dublin AE, Huxar A, Glass CA, Exlander MG;  
XX  
DR WPI; 2001-488969/53.  
XX  
DR N-PDB; AAD12793.  
XX  
PS New human VR3 receptor useful for the treatment of disorders including  
XX cancers arthritis and pain.  
XX  
XX Claim 11, Fig 8; 104pp; English.  
XX  
CC The patent relates to human vanilloid receptor VR3 polynucleotide and  
CC polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+  
CC have also been disclosed. The VR3 polypeptide is used to identify its  
CC modulators which are useful for the treatment of inflammatory conditions  
CC and for use as analgesics for intractable pain associated with  
CC postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex  
CC regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),  
CC as well as ulcers, neurodegenerative diseases, asthma, chronic

obstructive pulmonary disease, irritable bowel syndrome and psoriasis.  
The VR3 modulators are also useful for treatment of central nervous  
system (CNS) diseases, diseases of the intestinal tract, abnormal  
proliferation and cancer. The present sequence is human VR3 receptor  
isoform, VR3A+B+

Sequence 742 AA:

Query Match 100.0%; Score 3858; DB 4; Length 742;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGGEVAVELPGDSGTGGEAFPLSLIANLFEGBDGLSPSPADASHPAP 60
DB 1 MADSSGPRAGGEVAVELPGDSGTGGEAFPLSLIANLFEGBDGLSPSPADASHPAP 60
QY 61 GGRPNLRMKFOGAFKGVNPNIDLESTLYESSVPGKKA PMDSLFRYGYRRHSSN 120
DB 61 GGRPNLRMKFOGAFKGVNPNIDLESTLYESSVPGKKA PMDSLFRYGYRRHSSN 120
QY 121 KMRKKTIKOPQSPKAPAPPPILKVNRPILFDIVSRGSTADHDGLPLTHKKRL 180
DB 121 KMRKKTIKOPQSPKAPAPPPILKVNRPILFDIVSRGSTADHDGLPLTHKKRL 180
QY 181 TDEEFREPGTGTCLPKALLNSGRNDTIPVLLDIAERTGNMKEPINSPPFDIYRGQT 240
DB 181 TDEEFREPGTGTCLPKALLNSGRNDTIPVLLDIAERTGNMKEPINSPPFDIYRGQT 240
QY 241 ALHIAIERCKHVELLVAGADVAHQARFRPQDEGGYFRKGLPLSLA CTNPHI 300
DB 241 ALHIAIERCKHVELLVAGADVAHQARFRPQDEGGYFRKGLPLSLA CTNPHI 300
QY 301 VAVLTENPKKADMRQDSRGNTVLAALVAADNTRENTKFTVKKMYDLILKCARLEPDS 360
DB 301 VAVLTENPKKADMRQDSRGNTVLAALVAADNTRENTKFTVKKMYDLILKCARLEPDS 360
QY 361 NLEAVLNNDGLSLPMAAAKTGKIGIFOHIIIRREVTDETRHLSRKPKDVA YGVSYLYD 420
DB 361 NLEAVLNNDGLSLPMAAAKTGKIGIFOHIIIRREVTDETRHLSRKPKDVA YGVSYLYD 420
QY 421 LSLDLTCGEBA SVLEILVYNSKLENREHMAVEPINELADKKRKGA VSFYINVSYC 480
DB 421 LSLDLTCGEBA SVLEILVYNSKLENREHMAVEPINELADKKRKGA VSFYINVSYC 480
QY 481 AMVIFTLTAYOPLGEGTPPYRTVDYLRAGSVITLFTGVLPFFTNIKDLFMKCPGV 540
DB 481 AMVIFTLTAYOPLGEGTPPYRTVDYLRAGSVITLFTGVLPFFTNIKDLFMKCPGV 540
QY 541 NSLFDIDSGFOLLYFYSVLVIVSAALYLACIEAVLAVMFALVIGMNNALYFRGLKLTG 600
DB 541 NSLFDIDSGFOLLYFYSVLVIVSAALYLACIEAVLAVMFALVIGMNNALYFRGLKLTG 600
QY 601 TYSIMOKILFKDLFRLLVYLPMGYASALVSLNPCNNMVCNDONCVPYTPSC 660
DB 601 TYSIMOKILFKDLFRLLVYLPMGYASALVSLNPCNNMVCNDONCVPYTPSC 660
QY 661 ROSESTFTLLDIFKLTIGMDLEMLSTKYPVFIILVTYIILFVLLNMLALMGE 720
DB 661 ROSESTFTLLDIFKLTIGMDLEMLSTKYPVFIILVTYIILFVLLNMLALMGE 720
QY 721 TVGQVSKESHIMWLOSGRRRL 742
DB 721 TVGQVSKESHIMWLOSGRRRL 742

```

RESULT 2

AD181606 standard; protein; 831 AA.

AD181606;

22-APR-2004 (first entry)

Human vanilloid receptor-related channel protein #2.

Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;  
neurological disease; inflammatory disease; cancer; Alzheimer's disease;  
Parkinson's disease; asthma; rheumatoid arthritis; liver disease;  
hepatitis; cirrhosis; kidney disease; glomerulonephritis.

Homo sapiens.

US2004009537-A1.

15-JAN-2004.

13-JAN-2003; 2003US-00342844.

11-JAN-2002; 2002US-0347459P.

02-AUG-2002; 2002US-0401171P.

20-AUG-2002; 2002US-0405678P.

(ROOS/) ROOS J.

(STAU/) STAUDERMAN K.

(VELI/) VELICELEBI G.

Roos J, Stauderman K, Velicelebi G;

WPI; 2004-090465/09.

N-PSDB; AD181605.

Identifying an agent that modulates intracellular calcium levels, useful  
for treating diseases associated with calcium dysregulation (e.g.  
cancer), comprises monitoring the effects of the agent on store-operated  
calcium entry.

Disclosure; SEQ ID NO 76; 55pp; English.

The invention relates to identifying an agent that modulates  
intracellular calcium comprises monitoring the effects of the agent on  
store-operated calcium entry comprising contacting one or more test cells  
or their portion comprising one or more proteins that is (are) at least  
about 35% homologous to the protein encoded by Drosophila gene CG4536 or  
CG5842 over at least about 40% of the encoded protein (and that provides  
for store-operated calcium entry with a test agent), where the portion of  
the cell comprises the proteins, monitoring the effect(s) of the test  
compound on store-operated calcium entry and identifying a test agent as  
an agent if it has an effect on store-operated calcium entry. Also  
included are a method of modulating store-operated calcium entry  
(comprising modulating the level of, expression of, activity of or  
molecular interactions of a protein in a cell that has altered store-  
operated calcium entry, where the protein is at least about 35%  
homologous to the protein encoded by Drosophila gene CG4536 or CG5842  
over at least about 40% of the encoded protein and that provides for  
store-operated calcium entry, and where store-operated calcium transport  
into the cell is modulated) and a method of identifying a molecule that  
provides for store-operated calcium entry (comprising identifying a  
molecule that interacts with the protein mentioned above, thus,  
identifying molecules involved in modulating store-operated calcium  
entry. The protein does not contain the contiguous sequences appearing as  
entry. AD181644 and AD181645. The proteins are selected from ion transport  
proteins. The method is useful in modulating, or in identifying agents  
that modulate, intracellular calcium. These may be used in treating  
diseases associated with calcium dysregulation, such as neurodegenerative  
diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory  
diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases  
(e.g. hepatitis or cirrhosis) or kidney diseases (e.g. glomerulonephritis).  
The present sequence represents an identified  
homologue of one of the two above mentioned drosophila proteins.

Sequence 831 AA:

Query Match 99.2%; Score 3829; DB 8; Length 831;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 181 TDEEREPSTGKTC.PKALLINLSNGRNDTIPVLLDIAERTGNMRREFINSPPFDIYYRGQT 240  
 DB 181 TDEEREPSTGKTC.PKALLINLSNGRNDTIPVLLDIAERTGNMRREFINSPPFDIYYRGQT 240  
 QY 241 ALHIAIERCKKHVELLVAGADVAHAQARGFPOPEDEGGYFYFGBELPLSLAAGCTNOPIH 300  
 DB 241 ALHIAIERCKKHVELLVAGADVAHAQARGFPOPEDEGGYFYFGBELPLSLAAGCTNOPIH 300  
 QY 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLPDS 360  
 DB 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPMLMAAKTKGKIGIPOHIIIRREVTDERTHLSRKFKDMAAGPYVSSLYD 420  
 DB 361 NLEAVLNNDGLSPMLMAAKTKGKIGIPOHIIIRREVTDERTHLSRKFKDMAAGPYVSSLYD 420  
 QY 421 LSSLDTCGERASVLELVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYLIC 480  
 DB 421 LSSLDTCGERASVLELVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYLIC 480  
 QY 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540  
 DB 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540  
 QY 541 NSLFDGSPQLLYFYISVIVSAALYLAGIEAYLAVMVFALVIGMNAALYFTGKLITG 600  
 DB 541 NSLFDGSPQLLYFYISVIVSAALYLAGIEAYLAVMVFALVIGMNAALYFTGKLITG 600  
 QY 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 DB 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 QY 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
 DB 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
 QY 721 TVGVSKESKHIMKIQ 736  
 DB 721 TVGVSKESKHIMKIQ 736

## RESULT 4

AAG65787  
 ID AAG65787 standard; protein; 871 AA.

AC AAG65787;  
 DT 30-JAN-2002 (first entry)

DE Human ion channel VR-5 protein sequence.  
 XX

XX Ion channel; vanilloid receptor; VR-3; VR-5; nootropic; neuroprotective;  
 KW antiparkinsonian; analgesic; antidiabetic; antiproliferative; cytostatic;  
 KW antineumatic; antiarthritic; gene therapy; antitense therapy.

XX Homo sapiens.  
 OS

PN NO200168857-A2.  
 XX

PD 20-SEP-2001.  
 XX

PF 15-MAR-2001; 2001WO-US008329.  
 XX

PR 15-MAR-2000; 2000US-00525420.  
 XX

XX (MILL-) MILLENNIUM PHARM INC.  
 XX

PI Curtis RAD, Cook WJ;  
 XX

DR WPI; 2001-596911/67.  
 DR N-PSDB; AA166972; AA166973.

XX Nucleic acid encoding human ion channels referred to as Vanilloid  
 PT

PT receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or VR  
 PT -5 and for treating calcium homeostasis related disorders (e.g. dementia)  
 PT and pain disorders.  
 XX

PS Claim 13; Fig 2A-C; 167pp; English.

XX The invention provides nucleic acid encoding human ion channels referred  
 CC to as Vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can  
 CC be used to screen for naturally occurring VR-3 or VR-5 ligands or for  
 CC drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5  
 CC proteins and their modulators (e.g. antitense nucleic acids and anti-VR  
 CC antibodies) are useful for treating disorders characterized by  
 CC insufficient or excessive production of VR-3 or VR-5. These disorders are  
 CC calcium homeostasis related disorders (Alzheimer's disease, dementia,  
 CC Parkinson's disease), pain disorders (diabetic neuropathy, rheumatoid  
 CC arthritis) and/or cellular growth and/or proliferation disorders (e.g.  
 CC cancer). Numerous other examples of these disorders are given in the  
 CC specification. The present sequence represents the human VR-5

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 4; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPPAGGGEVAVELFGDSSGTGGEAFPLSLIANFEEDDGLSPSPADAPAP 60  
 DB 1 MADSSGPPAGGGEVAVELFGDSSGTGGEAFPLSLIANFEEDDGLSPSPADAPAP 60  
 QY 61 GGGEPVLRKKFQGAFFKGYVNPIDLESTLYESSVVPGRKAPMDSLPDYGYRHSSDN 120  
 DB 61 GGGEPVLRKKFQGAFFKGYVNPIDLESTLYESSVVPGRKAPMDSLPDYGYRHSSDN 120  
 QY 121 KRWREKKIIEKOPSPAPAPQPPPIIKVNRPIPLPIVSRGTAJDGLIPLLTKKTL 180  
 DB 121 KRWREKKIIEKOPSPAPAPQPPPIIKVNRPIPLPIVSRGTAJDGLIPLLTKKTL 180  
 QY 181 TDEEREPSTGKTC.PKALLINLSNGRNDTIPVLLDIAERTGNMRREFINSPPFDIYYRGQT 240  
 DB 181 TDEEREPSTGKTC.PKALLINLSNGRNDTIPVLLDIAERTGNMRREFINSPPFDIYYRGQT 240  
 QY 241 ALHIAIERCKKHVELLVAGADVAHAQARGFPOPEDEGGYFYFGBELPLSLAAGCTNOPIH 300  
 DB 241 ALHIAIERCKKHVELLVAGADVAHAQARGFPOPEDEGGYFYFGBELPLSLAAGCTNOPIH 300  
 QY 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLPDS 360  
 DB 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAONTRENTKFTYKMYDILLKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPMLMAAKTKGKIGIPOHIIIRREVTDERTHLSRKFKDMAAGPYVSSLYD 420  
 DB 361 NLEAVLNNDGLSPMLMAAKTKGKIGIPOHIIIRREVTDERTHLSRKFKDMAAGPYVSSLYD 420  
 QY 421 LSSLDTCGERASVLELVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYLIC 480  
 DB 421 LSSLDTCGERASVLELVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYLIC 480  
 QY 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540  
 DB 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRIAGEVITLFTGVLPFTNLIKDLFMKKCPGV 540  
 QY 541 NSLFDGSPQLLYFYISVIVSAALYLAGIEAYLAVMVFALVIGMNAALYFTGKLITG 600  
 DB 541 NSLFDGSPQLLYFYISVIVSAALYLAGIEAYLAVMVFALVIGMNAALYFTGKLITG 600  
 QY 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 DB 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 QY 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
 DB 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720



QY 721 TVGVSKSKHWLQ 736  
 DB 721 TVGVSKSKHWLQ 736

RESULT 5  
 AAU74935  
 ID AAU74935 standard; protein; 871 AA.

XX AAU74935;  
 AC  
 XX  
 DT 23-APR-2002 (first entry)

XX Amino acid sequence of human vanilloid receptor-like protein 2a (VR1-2a).

XX Human; vanilloid receptor-like protein 2a; VR1-2a; hypertension;  
 KM ion-channel protein; pain; osteoarthritis; diabetic neuropathy;  
 KM neuralgia; nerve injury; neurodegeneration; stroke; inflammation; asthma;  
 KM allergy; urogenital disorder; incontinence; hypotension;  
 KM perivascular disease; VR1-related disease; receptor.

XX Homo sapiens.

XX EP1160254-A1.

XX 05-DEC-2001.

XX 25-MAY-2001; 2001EP-00304663.

XX 31-MAY-2000; 2000US-0208156P.

XX (PF12) PFIZER INC.

XX Shinjo K, Yabuuchi H;

XX MPI: 2002-084359/12.

DR N-PSDB; ABK14002.

PT New human vanilloid receptor-like proteins, useful for identifying  
 PT modulators for e.g. treating pain, also related nucleic acid.

XX Claim 1; Page 17-18; 32pp; English.

XX The present invention relates to a new polypeptide that has a sequence  
 CC 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their  
 CC variants, as defined in the specification. The polypeptide of the  
 CC invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)  
 CC or 1900 base pairs (ABK14003) long, or their variants, also defined in  
 CC the specification. The polypeptides of the invention, which are human  
 CC vanilloid receptor-like (VR1) proteins, are used to identify specific  
 CC modulators that are potentially useful for treating pain (of any origin),  
 CC osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,  
 CC neurodegeneration, stroke, inflammation, asthma, allergy, urogenital  
 CC disorders, incontinence, hypo- or hyper-tension and perivascular disease.  
 CC The molecules of the invention can also be used to raise specific  
 CC antibodies. The nucleic acid that encodes the polypeptide of the  
 CC invention is useful for recombinant production of the protein and for  
 CC preparing transgenic animal models. The polypeptide, antibody and nucleic  
 CC acid of the invention are also useful as diagnostic agents for  
 CC determining (susceptibility to) VR1-related diseases. The present amino  
 CC acid sequence represents the human vanilloid receptor-like protein 2a  
 CC (VR1-2a) of the invention

CC Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;  
 Best Local Similarity 100.0%; Fred. No. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAVELPGDESGTPGCGAFPLSLIANFEGEDGSLSPSPADASRPAGP 60  
 DB 1 MADSSRGPRAGGEVAVELPGDESGTPGCGAFPLSLIANFEGEDGSLSPSPADASRPAGP 60

QY 61 GDGRPNLRKKFQGAFFKGVNPNIDLLSTLYESSVVPKAKMDSLFDYGYRRHSSDN 120  
 DB 61 GDGRPNLRKKFQGAFFKGVNPNIDLLSTLYESSVVPKAKMDSLFDYGYRRHSSDN 120  
 QY 121 KRRKKKIIKOPSPAPAPQPPPIIKVNRPIIPDIVSRGSTADLDGLIPILTHKKRL 180  
 DB 121 KRRKKKIIKOPSPAPAPQPPPIIKVNRPIIPDIVSRGSTADLDGLIPILTHKKRL 180  
 QY 181 TDEFRPEPTGKCLPKALLNLSNGRNDTIPVLDDIARTGNRREFINSFRRDIYYRGOT 240  
 DB 181 TDEFRPEPTGKCLPKALLNLSNGRNDTIPVLDDIARTGNRREFINSFRRDIYYRGOT 240  
 QY 241 ALHAIERRCKHYVELVVAQADVHAQARGFQPODEGGYFYFGEPLSLAAGTQPHI 300  
 DB 241 ALHAIERRCKHYVELVVAQADVHAQARGFQPODEGGYFYFGEPLSLAAGTQPHI 300  
 QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKYTKMYDLILKCARLPDS 360  
 DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKYTKMYDLILKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPIMAAATGKIGIHOHTIRREPTDEDRIHSRKRDMAYGVYSLYD 420  
 DB 361 NLEAVLNNDGLSPIMAAATGKIGIHOHTIRREPTDEDRIHSRKRDMAYGVYSLYD 420  
 QY 421 LSLDTCGEASYLEILVYNSKIENHEMLAVEPINELDKMRKFGAVSYINVSYLQ 480  
 DB 421 LSLDTCGEASYLEILVYNSKIENHEMLAVEPINELDKMRKFGAVSYINVSYLQ 480  
 QY 481 AMVIFTLTAYYQPLESTPEYPTRTTYDYLRLAGEVITLTGVLFFFTNIDKLFMKKCPGV 540  
 DB 481 AMVIFTLTAYYQPLESTPEYPTRTTYDYLRLAGEVITLTGVLFFFTNIDKLFMKKCPGV 540  
 QY 541 NSLFTDGSFQLYFYISVAVTSAALVLAGIEAYLAVMPFALVIGMNNALYFRGKLTG 600  
 DB 541 NSLFTDGSFQLYFYISVAVTSAALVLAGIEAYLAVMPFALVIGMNNALYFRGKLTG 600  
 QY 601 TYSIMIOKILFQDLFRFLVYLLFMIGYASALVSLNCPANKKVCNEQDQNTCTVTPYSPC 660  
 DB 601 TYSIMIOKILFQDLFRFLVYLLFMIGYASALVSLNCPANKKVCNEQDQNTCTVTPYSPC 660  
 QY 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYVVFIIILVYIILTFVILLNMLIALMGE 720  
 DB 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYVVFIIILVYIILTFVILLNMLIALMGE 720  
 QY 721 TVGVSKSKHWLQ 736  
 DB 721 TVGVSKSKHWLQ 736

RESULT 6  
 ABB79191  
 ID ABB79191 standard; protein; 871 AA.

XX ABB79191;

XX 07-AUG-2002 (first entry)

XX Human VR4 protein SEQ ID NO:2.

XX Human; VR4; vanilloid 4 receptor; receptor; osteopathic; anti-rheumatic;  
 KM antiautarchic; vulnerability; analgesic; gene therapy; cartilage; bone;  
 KM larynx; auditory canal; intravertebral disc; ligament; tendon;  
 KM joint capsule; bone development disorder; osteoporosis; osteoarthritis;  
 KM joint destruction; rheumatoid arthritis.

XX Homo sapiens.

XX WO200234280-A2.

XX 02-MAY-2002.

XX 25-OCT-2001; 2001WO-GB004739.

PR 25-OCT-2000; 2000GB-00026114.  
 XX (SMIX ) SMITHKLINE BEECHAM PLC.  
 PA Davis JB, Gunthorpe MJ, Egerton J, Smart D;  
 PI WPI: 2002-471426/50.  
 XX N-PSDB; ABB67645.  
 DR  
 XX Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of  
 PT the polypeptide or an antisense polynucleotide to the polynucleotide, for  
 PT manufacture of a medicament for treating cartilage and/or bone diseases.  
 XX  
 PS Claim 8; Page 22; 30pp; English.  
 XX  
 CC The present sequence represents human vanilloid 4 receptor (VR4). VR4 has  
 CC osteopathic, antirheumatic, antiarthritic, vulnary and analgesic  
 CC activities. VR4 proteins and polynucleotide sequences can be used in  
 CC modulating VR4 activity, in gene therapy and in antisense gene therapy.  
 CC VR4 is useful for the manufacture of a medicament for treating diseases  
 CC of cartilage and/or bone, or for the treatment of pain associated with  
 CC it, where the disease is one affecting the larynx, auditory canal,  
 CC intervertebral discs, ligaments, tendons and joint capsules, or a disease  
 CC associated with bone development including osteoporosis, or diseases  
 CC involving joint destruction such as rheumatoid arthritis or  
 CC osteoarthritis, and the pain is associated with rheumatoid arthritis or  
 CC osteoarthritis  
 XX  
 SQ Sequence 871 AA;  
 XX  
 Query Match 99.2%; Score 3829; DB 5; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAOSSSEPRAGPGEVVALPDESGTPGGEAFPLSLANLFEGRDGSLSPPADSRPAGP 60  
 DB 1 MAOSSSEPRAGPGEVVALPDESGTPGGEAFPLSLANLFEGRDGSLSPPADSRPAGP 60  
 QY 61 GDGEPNLRMKGQAFRGKGVNPIDLESTLYESSVVGPKKAPMDSLFDTYRHHSSDN 120  
 DB 61 GDGEPNLRMKGQAFRGKGVNPIDLESTLYESSVVGPKKAPMDSLFDTYRHHSSDN 120  
 QY 121 KRWKRTKIEKOPQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLPLLTTHKKRL 180  
 DB 121 KRWKRTKIEKOPQSPKAPAPPPILKVNRPILFDIVSRGSTADLDGLPLLTTHKKRL 180  
 QY 181 TDEFREPSSTGKTLCPKALNLSNGRNDTIVLDIARNGMGEFINSPPRDITYRGQT 240  
 DB 181 TDEFREPSSTGKTLCPKALNLSNGRNDTIVLDIARNGMGEFINSPPRDITYRGQT 240  
 QY 241 ALHAIERRCHGYVELVAQAGADVAHQARGFPOKDEGFGYFGEPLSLAICTNPHI 300  
 DB 241 ALHAIERRCHGYVELVAQAGADVAHQARGFPOKDEGFGYFGEPLSLAICTNPHI 300  
 QY 301 VNYLTENPHKADNRDQSRGNTVLAHVAIADNTRENTKFTVTMTDLILKCARLPDS 360  
 DB 301 VNYLTENPHKADNRDQSRGNTVLAHVAIADNTRENTKFTVTMTDLILKCARLPDS 360  
 QY 361 NLEAVANNDSPLMMAKTKGTIGFOHIRREVTDERTLSKRFKDMAGPYSSLYD 420  
 DB 361 NLEAVANNDSPLMMAKTKGTIGFOHIRREVTDERTLSKRFKDMAGPYSSLYD 420  
 QY 421 LLSLDTGCEASVLEIIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVSYLC 480  
 DB 421 LLSLDTGCEASVLEIIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFINVSYLC 480  
 QY 481 AMVIFLTAYVQPLEGTPPYRYRTVDYLRLAGEVITLFTGVLPFFTNIKDLFMKKCPGV 540  
 DB 481 AMVIFLTAYVQPLEGTPPYRYRTVDYLRLAGEVITLFTGVLPFFTNIKDLFMKKCPGV 540  
 QY 541 NSLFIIDSGFOLLVYTVVSALVYAGTBAVYANVWVPLVGMNVALFTFGKLTG 600  
 DB 541 NSLFIIDSGFOLLVYTVVSALVYAGTBAVYANVWVPLVGMNVALFTFGKLTG 600

QY 601 TYSIMIOKILFKDLFRFELLVYLFMIGYASALVSLNPNCKMKNEDQNTCTVPTPSC 660  
 DB 601 TYSIMIOKILFKDLFRFELLVYLFMIGYASALVSLNPNCKMKNEDQNTCTVPTPSC 660  
 QY 661 RDSERTSTFLDLFKTLTGMDLEMLSTKYPVFIILVTVIILFVILLNMLLMGE 720  
 DB 661 RDSERTSTFLDLFKTLTGMDLEMLSTKYPVFIILVTVIILFVILLNMLLMGE 720  
 QY 721 TWGVSKESKHIWKLQ 736  
 DB 721 TWGVSKESKHIWKLQ 736  
 RESULT 7  
 ADG64947  
 ID ADG64947 standard; protein; 871 AA.  
 AC ADG64947;  
 XX 11-MAR-2004 (first entry)  
 DT  
 XX VANILREP4 polypeptide of the invention.  
 DE  
 XX vanilrep4; VR4; Analgesic; cerebroprotective; antiinflammatory;  
 KW antidiabetic; anorectic; vasotrophic; uterachic; ischemia;  
 KW neurodegeneration; inflammatory disorder; irritable bowel syndrome;  
 KW diabetes; obesity.  
 XX  
 XX Homo sapiens.  
 OS  
 XX EPI170365-A1.  
 XX 09-JAN-2002.  
 PD  
 XX 04-JUL-2000; 2000EP-00202352.  
 PF  
 XX 04-JUL-2000; 2000EP-00202352.  
 PR  
 XX (SMIX ) SMITHKLINE BEECHAM PLC.  
 PA Smith G, Hayes PD, Smart D, Davis JB, Kelsell RE;  
 PI WPI: 2002-156636/21.  
 DR N-PSDB; ADG64946.  
 XX  
 PT Polypeptide of ion channel family polypeptides, designated vanilrep4,  
 PT useful as a vaccine for inducing immune response against diseases such as  
 PT neuropathies, algesia, nerve injury, ischemia, stroke, incontinence,  
 PT diabetes, obesity.  
 XX  
 PS Claim 1; SEQ ID NO 2; 29pp; English.  
 XX  
 CC The present invention relates to a polypeptide of ion channel family  
 CC polypeptides, vanilrep4 (VR4). The peptides are useful for treating pain  
 CC (e.g. chronic pain, neuropathic pain, post-operative pain, rheumatoid  
 CC arthritic pain), neuralgia, neuropathies, algesia, nerve injury,  
 CC ischemia, neurodegeneration, stroke, incontinence, inflammatory  
 CC disorders, irritable bowel syndrome, diabetes or obesity. Fragments of  
 CC the protein are useful for producing full-length polypeptides by peptide  
 CC synthesis therefore the variants may also be employed as intermediate for  
 CC producing full-length polypeptide. The proteins are also useful for  
 CC identifying agonists or antagonists of peptide activity and expression.  
 CC The peptide is useful as diagnostic reagents for diagnosing a disease or  
 CC a susceptibility to a disease by detecting mutations in the associated  
 CC gene, and is also useful for chromosome localization studies and tissue  
 CC expression studies. The peptide is useful for producing transgenic  
 CC animals, which include knock-in animals (in which an animal gene is  
 CC replaced by human equivalent within the genome of the animal), useful in  
 CC drug discovery process, for target validation, where the compound is  
 CC specific for human target. Peptides and Ab is useful for configuring  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA in cells. The peptides are useful as vaccines for

including an immunological response in a mammal. The present sequence  
 CC represents VANILRP4 polypeptide.

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
QY 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRRHSSDN 120
DB 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRRHSSDN 120
QY 121 KMRKKKIIKOPQSPKAPAPOPPPILKVFNRPIILFDIVSRGSTADLDGLPLTLTKKRL 180
DB 121 KMRKKKIIKOPQSPKAPAPOPPPILKVFNRPIILFDIVSRGSTADLDGLPLTLTKKRL 180
QY 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFINSFPDIYYRGOT 240
DB 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFINSFPDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVAHQARGRFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
DB 241 ALHIAIERCKHYVELLVAQADVAHQARGRFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNTRENTKFTYKMDLLKCARLPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNTRENTKFTYKMDLLKCARLPDS 360
QY 361 NLEAVLNDGSLPMAAAKTGIGIFQHIIRREVTEDTRHLSRKKCKDWAAGPVYSLYD 420
DB 361 NLEAVLNDGSLPMAAAKTGIGIFQHIIRREVTEDTRHLSRKKCKDWAAGPVYSLYD 420
QY 421 LSSLDTCGEBASVLELVNLSKIENHEMLAVEPINELLRDKWRKFGAASFYINVSYL 480
DB 421 LSSLDTCGEBASVLELVNLSKIENHEMLAVEPINELLRDKWRKFGAASFYINVSYL 480
QY 481 ANVIFLTVAYOPLBETPPYPTWYDLRIAGEVITLFTGVLPFTNTKDLPMKCCPV 540
DB 481 ANVIFLTVAYOPLBETPPYPTWYDLRIAGEVITLFTGVLPFTNTKDLPMKCCPV 540
QY 541 NSLFLDGSFQLLYFIYSVIVISAALYLAGIEAYLAVMFAVLGMNNALEFTRGLKLTG 600
DB 541 NSLFLDGSFQLLYFIYSVIVISAALYLAGIEAYLAVMFAVLGMNNALEFTRGLKLTG 600
QY 601 TYSIMIQKILFKDLFFELLYLLEFMGYASALVSLINPCANMKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIQKILFKDLFFELLYLLEFMGYASALVSLINPCANMKVCNEDQTNCTVPTPSC 660
QY 661 RDSFESTFLDLFLKLTIGMDLEMLSKRPVVFILLYVYIILTFVLLNMLTALMGE 720
DB 661 RDSFESTFLDLFLKLTIGMDLEMLSKRPVVFILLYVYIILTFVLLNMLTALMGE 720
QY 721 TVGQVSKESKIMKIQ 736
DB 721 TVGQVSKESKIMKIQ 736

```

RESULT 8

ID ADG32562

ADG32562 standard; protein; 871 AA.

AC ADG32562;

XX 26-FEB-2004 (first entry)

DE Human TRPV4 protein, member of the vanilloid receptor family.

XX human; vanilloid receptor; VR; pain perception; TRPV3; VR1S; VR4;

KM TRPV7, TRPV4; VR13; OTRPC4; TRPM8; TRPX; trkA; inflammation;  
 KM skin disorder; cancer; analgesic; antiinflammatory; dermatological;  
 KM cytostatic.

OS Homo sapiens.

PN WO2002101045-A2.

XX 19-DEC-2002.

PD 13-JUN-2002; 2002WO-EP065520.

XX 13-JUN-2001; 2001US-0297835P.

PR 22-JAN-2002; 2002US-0351238P.

PR 29-JAN-2002; 2002US-0352914P.

PR 12-FEB-2002; 2002US-0357161P.

PR 15-MAY-2002; 2002US-0381086P.

PR 16-MAY-2002; 2002US-0381739P.

PA (NOV ) NOVARTIS AG.

PA (IRMT-) IRM LLC.

PI Patapoutian A, Song C, Ganju P, Peier A, McIntyre P, Bevan S;

DR WPI; 2003-156962/15.

XX N-PSDB; ADG32561.

PT New isolated TRPV3, TRPV4 or TRPM8 vanilloid receptor nucleic acid

PT molecule and polypeptides, useful for the diagnosis and treatment of

PS disorders such as pain, inflammation, skin diseases and cancer.

XX Claim 69; SEQ ID NO 17; 197pp; English.

This invention relates to novel vanilloid receptor (VR) related nucleic  
 acids and encoded proteins thereof. Specifically, it refers to certain  
 members of the VR family that are involved in pain perception, in  
 particular, TRPV3 (previously known as VR1S, VR4, VR4 & TRPV7), TRPV4  
 (previously known as VR13 & OTRPC4) and TRPM8 (previously known as TRPX).  
 Furthermore, this invention includes trkA pain specific genes expressed  
 in the sensory neurons of the dorsal root ganglia. Accordingly, such  
 compositions can be useful for the diagnosis, treatment and prevention of  
 pain, inflammation, skin disorders and cancer, and so exhibit analgesic,  
 antiinflammatory, dermatological and cytostatic activities. This  
 polypeptide sequence is the human TRPV4 protein of the invention.

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 7; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPGDESGTGGGAFFPLSLANLEGGEDGSLSPSPADASRPAGP 60
QY 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRRHSSDN 120
DB 61 GDRPNLRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRRHSSDN 120
QY 121 KMRKKKIIKOPQSPKAPAPOPPPILKVFNRPIILFDIVSRGSTADLDGLPLTLTKKRL 180
DB 121 KMRKKKIIKOPQSPKAPAPOPPPILKVFNRPIILFDIVSRGSTADLDGLPLTLTKKRL 180
QY 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFINSFPDIYYRGOT 240
DB 181 TDEEFREPGTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREFINSFPDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVAHQARGRFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
DB 241 ALHIAIERCKHYVELLVAQADVAHQARGRFQPKDEGGYFFGELPLSLAAGCTNQPPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNTRENTKFTYKMDLLKCARLPDS 360

```

Db 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDLILKCARLPDS 360  
 Qy 361 NLEAVLNNDGLSPMAAAKTGKIGIFOHIIIRREVTDEDRHLSRKPKDMAVGPVYSSLYD 420  
 Db 361 NLEAVLNNDGLSPMAAAKTGKIGIFOHIIIRREVTDEDRHLSRKPKDMAVGPVYSSLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480  
 Qy 481 AMVITLTAYYQPLEGTPPYPTTYDYRLAGEVITLFFGVLPFTNKKDLFMKCPGV 540  
 Db 481 AMVITLTAYYQPLEGTPPYPTTYDYRLAGEVITLFFGVLPFTNKKDLFMKCPGV 540  
 Qy 541 NSLFDGSPQLVFTYISVLYSALYIAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600  
 Db 541 NSLFDGSPQLVFTYISVLYSALYIAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600  
 Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFITLVTYIILTFVLLNMLALMGE 720  
 Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFITLVTYIILTFVLLNMLALMGE 720  
 Qy 721 TVGQVSKESKHIMKLQ 736  
 Db 721 TVGQVSKESKHIMKLQ 736

RESULT 9  
 ID ADL71047 standard; protein; 871 AA.

AC ADL71047;  
 DT 20-MAY-2004 (first entry)

XX Type II collagen expression promoting protein, seq id 40.

XX Osteopathic; antiinflammatory; antirheumatic; antiarthritic;  
 KM gene therapy; type II collagen; expression; cartilage disease;  
 XX osteoarthritis; cartilage defect; rheumatoid arthritis; human.

OS Homo sapiens.

XX W02003087375-A1.

XX 23-OCT-2003.

XX 16-APR-2003; 2003WO-JP004802.

XX 16-APR-2002; 2002JP-00113908.

XX 19-APR-2002; 2002US-0373594P.

XX (ASAH ) ASAH KASEI KK.

XX Matsuda A, Honda G, Muramatsu S;

XX WPI; 2003-845331/78.

XX N-PSDB; ADL71046.

XX New purified protein that promotes type II collagen expression, useful

XX for preventing and treating a cartilage disease, e.g. osteoarthritis,

XX cartilage defect, or rheumatoid arthritis.

XX Claim 1; SEQ ID NO 40; 271pp; English.

CC ingredient. The proteins, genes, agents and methods are useful for  
 CC preventing and treating a cartilage disease, e.g. osteoarthritis,  
 CC cartilage defect, or rheumatoid arthritis. The current sequence  
 CC represents a human protein that promotes type II collagen expression.

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 7; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPEVAVELPDGSGTPGGAFLSSIANIPEGDGLSPSPAPASPAGE 60  
 Db 1 MADSSGPRAGPEVAVELPDGSGTPGGAFLSSIANIPEGDGLSPSPAPASPAGE 60  
 Qy 61 GDRPMLRMKFGAFKGPVNPIDLESTLYESSVVPGRPKAMDSLFYGYRRHSSDN 120  
 Db 61 GDRPMLRMKFGAFKGPVNPIDLESTLYESSVVPGRPKAMDSLFYGYRRHSSDN 120  
 Qy 121 KRRRKXIEKQPSAPAPQPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180  
 Db 121 KRRRKXIEKQPSAPAPQPPILKVNRPILFDIVSRGSTADLDGLPFLTHKKRL 180  
 Qy 181 TDEEPEPSTGKTCLEKALLNLSNGRNDTIPVLDIAERTGNRREFINSFPRDIYRGOT 240  
 Db 181 TDEEPEPSTGKTCLEKALLNLSNGRNDTIPVLDIAERTGNRREFINSFPRDIYRGOT 240  
 Qy 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFYFGLPLSLAACTNQPHI 300  
 Db 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFYFGLPLSLAACTNQPHI 300  
 Qy 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDLILKCARLPDS 360  
 Db 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTYKMYDLILKCARLPDS 360  
 Qy 361 NLEAVLNNDGLSPMAAAKTGKIGIFOHIIIRREVTDEDRHLSRKPKDMAVGPVYSSLYD 420  
 Db 361 NLEAVLNNDGLSPMAAAKTGKIGIFOHIIIRREVTDEDRHLSRKPKDMAVGPVYSSLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDKMRKGAVSFYINVSYL 480  
 Qy 481 AMVITLTAYYQPLEGTPPYPTTYDYRLAGEVITLFFGVLPFTNKKDLFMKCPGV 540  
 Db 481 AMVITLTAYYQPLEGTPPYPTTYDYRLAGEVITLFFGVLPFTNKKDLFMKCPGV 540  
 Qy 541 NSLFDGSPQLVFTYISVLYSALYIAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600  
 Db 541 NSLFDGSPQLVFTYISVLYSALYIAGIEAVLAVMVFALVGMNNALYFRGLKLTG 600  
 Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFITLVTYIILTFVLLNMLALMGE 720  
 Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFITLVTYIILTFVLLNMLALMGE 720  
 Qy 721 TVGQVSKESKHIMKLQ 736  
 Db 721 TVGQVSKESKHIMKLQ 736

RESULT 10  
 ID ADI81584 standard; protein; 871 AA.

AC ADI81584;

DT 22-APR-2004 (first entry)

DE Human vanilloid receptor-related channel like protein.

XX Human; calcium entry modulator; CD4536; intracellular calcium;  
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;  
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;  
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.  
 OS Homo sapiens.  
 PN US2004009537-A1.  
 XX  
 PD 15-JAN-2004.  
 XX  
 PF 13-JAN-2003; 2003US-00342844.  
 XX  
 PR 11-JAN-2002; 2002US-0347459P.  
 XX  
 PR 02-AUG-2002; 2002US-0401171P.  
 PR 20-AUG-2002; 2002US-0405678P.  
 XX  
 PA (ROOS/) ROOS J.  
 PA (STAU/) STAUDERMAN K.  
 PA (VELI/) VELICELEBI G.  
 XX  
 PI Roos J, Stauderman K, Velicelebi G;  
 XX  
 DR WEI; 2004-090465/09.  
 DR N-PDB; AD181583.  
 XX  
 PT Identifying an agent that modulates intracellular calcium levels, useful  
 PT for treating diseases associated with calcium dysregulation (e.g.  
 PT cancer), comprises monitoring the effects of the agent on store-operated  
 PT calcium entry.  
 XX  
 PS Disclosure; SEQ ID NO 54; 55pp; English.  
 XX  
 CC The invention relates to identifying an agent that modulates  
 CC intracellular calcium comprising monitoring the effects of the agent on  
 CC store-operated calcium entry comprising contacting one or more test cells  
 CC or their portion comprising one or more proteins that is (are) at least  
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or  
 CC CG5842 over at least about 40% of the encoded protein (and that provides  
 CC for store-operated calcium entry with a test agent), where the portion of  
 CC the cell comprises the proteins, monitoring the effect(s) of the test  
 CC compound on store-operated calcium entry and identifying a test agent as  
 CC an agent if it has an effect on store-operated calcium entry. Also  
 CC included are a method of modulating store-operated calcium entry  
 CC (comprising modulating the level of expression of, activity of or  
 CC molecular interactions of a protein in a cell that has altered store-  
 CC operated calcium entry, where the protein is at least about 35%  
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842  
 CC over at least about 40% of the encoded protein and that provides for  
 CC store-operated calcium entry, and where store-operated calcium transport  
 CC into the cell is modulated) and a method of identifying a molecule that  
 CC provides for store-operated calcium entry (comprising identifying a  
 CC molecule that interacts with the protein mentioned above, thus,  
 CC identifying molecules involved in modulating store-operated calcium  
 CC entry. The protein does not contain the contiguous sequences appearing as  
 CC AD181644 and AD181645. The proteins are selected from ion transport  
 CC proteins. The method is useful in modulating, or in identifying agents  
 CC that modulate, intracellular calcium. These may be used in treating  
 CC diseases associated with calcium dysregulation, such as neurodegenerative  
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory  
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases  
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.  
 CC glomerulonephritis). The present sequence represents an identified  
 CC homologue of one of the two above mentioned drosophila proteins.  
 XX  
 SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 8; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MADSSGPRAGPGEVAVELPDDESGTGGGEAFPLSSILANLFEGBDGSISPSPADASRPAGP 60

DB 1 MADSSGPRAGPGEVAVELPDDESGTGGGEAFPLSSILANLFEGBDGSISPSPADASRPAGP 60  
 QY GDERPVLRMKFOGAFKRGVNPIDLESTLYESSVGPCKAMDSIFDGTGRHSSDN 120  
 DB 61 GDERPVLRMKFOGAFKRGVNPIDLESTLYESSVGPCKAMDSIFDGTGRHSSDN 120  
 QY KRWKRIIEKOPSPAPAPQPPILKVENRPIILFDIVSRGSTADLDGLPFLTHKKRL 180  
 DB 121 KRWKRIIEKOPSPAPAPQPPILKVENRPIILFDIVSRGSTADLDGLPFLTHKKRL 180  
 QY 121 KRWKRIIEKOPSPAPAPQPPILKVENRPIILFDIVSRGSTADLDGLPFLTHKKRL 180  
 DB 121 KRWKRIIEKOPSPAPAPQPPILKVENRPIILFDIVSRGSTADLDGLPFLTHKKRL 180  
 QY 181 TDEEPREPSTGKTCLEPKALNLSNGRNDTIPVLLDIAERTGNREIFNSPFDIYYRGQT 240  
 DB 181 TDEEPREPSTGKTCLEPKALNLSNGRNDTIPVLLDIAERTGNREIFNSPFDIYYRGQT 240  
 QY 241 ALHIALERRCKHYVELLVAGADVAHQARRFQPPDEGGYFFGELPLSLAQTQPHI 300  
 DB 241 ALHIALERRCKHYVELLVAGADVAHQARRFQPPDEGGYFFGELPLSLAQTQPHI 300  
 QY 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAENTRENTKFTYKMTDLLKCARLPDS 360  
 DB 301 VNYLTENPHKKADMRRODSRGNTVLAHVAIAENTRENTKFTYKMTDLLKCARLPDS 360  
 QY 361 NLEAVINNDGLSPDMAAKTKIGIFQHIIRREVTDETRHLSRKKDMAVGPVYSSLYD 420  
 DB 361 NLEAVINNDGLSPDMAAKTKIGIFQHIIRREVTDETRHLSRKKDMAVGPVYSSLYD 420  
 QY 421 LSSLDCGGEASVLELVNYSKIENHMLAVPINELLRDKRKGAVSFYNNVYLC 480  
 DB 421 LSSLDCGGEASVLELVNYSKIENHMLAVPINELLRDKRKGAVSFYNNVYLC 480  
 QY 481 AMVIFTLTAYVOPLEGTPPYPTTYDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV 540  
 DB 481 AMVIFTLTAYVOPLEGTPPYPTTYDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV 540  
 QY 541 NSIFIDSGQLLYFTIVTSALYLAGIEAYLAVMPALVGMNNAVYFRGLKLTG 600  
 DB 541 NSIFIDSGQLLYFTIVTSALYLAGIEAYLAVMPALVGMNNAVYFRGLKLTG 600  
 QY 601 TVSIMOKLFLKDFLFLVYLLEFMIGVASALVSLNPCNMVKNVEDQNCVPPYPSG 660  
 DB 601 TVSIMOKLFLKDFLFLVYLLEFMIGVASALVSLNPCNMVKNVEDQNCVPPYPSG 660  
 QY 661 RDEETSTFLDLFLKLTIGGDEMLSTKYPVVFTLLVYIILFEVLLNMLIALMGE 720  
 DB 661 RDEETSTFLDLFLKLTIGGDEMLSTKYPVVFTLLVYIILFEVLLNMLIALMGE 720  
 QY 721 TVGQVSKESKHMKLQ 736  
 DB 721 TVGQVSKESKHMKLQ 736  
 RESULT 11  
 AD181608  
 ID AD181608 standard; protein; 871 AA.  
 XX  
 AC AD181608;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human OTRPC4 cation channel.  
 XX  
 XX Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;  
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;  
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;  
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004009537-A1.  
 PD 15-JAN-2004.  
 XX

13-JAN-2003; 2003US-00342844 .  
11-JAN-2002; 2002US-0347459P .  
02-AUG-2002; 2002US-0401171P .  
20-AUG-2002; 2002US-0405678P .  
(ROOS/) ROOS J .  
(STAU/) STAUDERMAN K .  
(VELI/) VELICELEBI G .  
Roos J, Stauderman K, Velicelebi G;  
MPI; 2004-090465/09 .  
N-PSDB; ADI81607 .  
Identifying an agent that modulates intracellular calcium levels, useful  
for treating diseases associated with calcium dysregulation (e.g.  
cancer), comprises monitoring the effects of the agent on store-operated  
calcium entry .  
Disclosure; SEQ ID NO 78; 55pp; English .  
The invention relates to identifying an agent that modulates  
intracellular calcium comprising monitoring the effects of the agent on  
store-operated calcium entry comprising contacting one or more test cells  
or their portion comprising one or more proteins that is (are) at least  
about 35% homologous to the protein encoded by Drosophila gene CG4536 or  
CG5842 over at least about 40% of the encoded protein (and that provides  
for store-operated calcium entry with a test agent), where that portion of  
the cell comprises the proteins, monitoring the effect(s) of the test  
compound on store-operated calcium entry and identifying a test agent as  
an agent if it has an effect on store-operated calcium entry . Also  
included are a method of modulating store-operated calcium entry  
(comprising modulating the level of, expression of, activity of or  
molecular interactions of a protein in a cell that has altered store-  
operated calcium entry, where the protein is at least about 35%  
homologous to the protein encoded by Drosophila gene CG4536 or CG5842  
over at least about 40% of the encoded protein and that provides for  
store-operated calcium entry, and where store-operated calcium transport  
into the cell is modulated) and a method of identifying a molecule that  
provides for store-operated calcium entry (comprising identifying a  
molecule that interacts with the protein mentioned above, thus,  
identifying molecules involved in modulating store-operated calcium  
entry . The protein does not contain the contiguous sequences appearing as  
ADI81644 and ADI81645 . The proteins are selected from ion transport  
proteins . The method is useful in modulating, or in identifying agents  
that modulate, intracellular calcium . These may be used in treating  
diseases associated with calcium dysregulation, such as neurodegenerative  
diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory  
diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases  
(e.g. hepatitis or cirrhosis) or kidney diseases (e.g.  
glomerulonephritis) . The present sequence represents an identified  
homologue of one of the two above mentioned drosophila proteins .  
Sequence 871 AA;

Query Match	Similarity	99.2%	Score	3829;	DB	8;	Length	871;	
Beet	Local	Similarity	100.0%	Pred.	No.	0;			
Matches	736;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MADSSSEGPRAGPGEVAHLPGDESTGPGGEAPPLSLANI,FEGEDSLSPSPADASPAGP	60						
Db	1	MADSSSEGPRAGPGEVAHLPGDESGTPGGEAPPLSLANL,FEGEDSLSPSPADASPAGP	60						
Qy									
Db									
Qy	61	GDGRPNLMMKTOGAAFRKGVPNPDLLESTLYHSSVYPPGPKAPMMSLPDYGYRRHSSDN	120						
Db	61	GDGRPNLMMKTOGAERKGVPNPIDLLESTLYESSVVPKAPMMSLPDYGYRRHSSDN	120						
Qy									
Db									
Qy	121	KWRKRKTIEXKQPOSFKAPAPQPPILTKYFNRPILFDIYSRGSGTADLDGLPFLTLTHKKRL	180						
Db	121	KWRKRKTIEXKQPOSFKAPAPQPPILTKYFNRPILFDIYSRGSGTADLDGLPFLTLTHKKRL	180						
Qy									
Db									
Qy	181	TDEERFESTGKYTCLPKALINLSNGRNDTIPVLLDIARTGNMREEIFNSPFDIYYRCQT	240						

Db	181	TDEEFREPSTGKTCLEPKALLNLSNGRNTTIPVLDAIRTGNMREEFINSPEPRDIYVAGQT	240
Qy	241	ALHIALERRCKRIYVELLVAAQGDVVAQARGRFEPQKQGGFYFGCELPLSLAATQNPPI	3000
Db	241	ALHIALERRCKRIYVELLVAAQGDVVAQARGRFEPQKQGGFYFGCELPLSLAATQNPPI	3000
Qy	301	VNYLTENPKKADMRKODSRGNTVHALVALADNTRENTKFTVMQYDLLLLKCARLPDS	3600
Db	301	VNYLTENPKKADMRKODSRGNTVHALVALADNTRENTKFTVMQYDLLLLKCARLPDS	3600
Qy	361	NLEAVINDGSLPMMAAATGKIGIFQHIIRRETVDEDTRLSKRFQDAVGPYSSLYD	4200
Db	361	NLEAVINDGSLPMMAAATGKIGIFQHIIRRETVDEDTRLSKRFQDAVGPYSSLYD	4200
Qy	421	LSSLDTQGBEASVLEILVYNSKLEIKRHHMLAVEPINELDRDKMRKFGAVSFYINVASYL	4800
Db	421	LSSLDTQGBEASVLEILVYNSKLEIKRHHMLAVEPINELDRDKMRKFGAVSFYINVASYL	4800
Qy	481	AMVIFTLIAYQPLRGTPRPYPRTTVDYLRLAGEVILFTGVLEFFTNIKOLFEMKCPGV	5400
Db	481	AMVIFTLIAYQPLRGTPRPYPRTTVDYLRLAGEVILFTGVLEFFTNIKOLFEMKCPGV	5400
Qy	541	NSLFIQSGPOLLYFTSYSTVYSAALYLAGI EAYLVAVVFPALVGMNNALEFRGLGTG	6000
Db	541	NSLFIQSGPOLLYFTSYSTVYSAALYLAGI EAYLVAVVFPALVGMNNALEFRGLGTG	6000
Qy	601	TVSIMGLOKILFKDLFRFLVYLFLPMIGYASALVSLNLCANMKVCNEDQNTCTVPTPSC	6600
Db	601	TVSIMGLOKILFKDLFRFLVYLFLPMIGYASALVSLNLCANMKVCNEDQNTCTVPTPSC	6600
Qy	661	RDESETSTFLDLFKLTIQMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMG	7200
Db	661	RDESETSTFLDLFKLTIQMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMG	7200
Qy	721	TVGQVSKESGHIIMKLG 736	
Db	721	TVGQVSKESGHIIMKLG 736	

RESULT 12	
AD181588	
ID	AD181588 standard; protein; 871 AA.
XX	
AC	AD181588;
XX	
DT	22-APR-2004 (first entry)
DE	Human vanilloid receptor-like channel 2.
XX	
KW	Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
KW	neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW	Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW	hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX	
OS	Homo sapiens.
XX	
FN	US2004009537-A1.
XX	
PD	15-JAN-2004.
XX	
PF	13-JAN-2003; 2003US-00342844.
XX	
PR	11-JAN-2002; 2002US-0347459P.
PR	02-AUG-2002; 2002US-0401171P.
PR	20-AUG-2002; 2002US-0405678P.
XX	
PA	(ROOS/) ROOS J.
PA	(STAU/) STAUDERMAN K.
PA	(VELI/) VELICELEBI G.
XX	
PI	Roos J, Stauderman K, Velicelebi G;
XX	



DR WPI: 2004-090465/09.  
 DR N-PSDB; ADI81587.  
 PT Identifying an agent that modulates intracellular calcium levels, useful  
 PT for treating diseases associated with calcium dysregulation (e.g.  
 PT cancer), comprises monitoring the effects of the agent on store-operated  
 PT calcium entry.  
 XX  
 XX Disclosure; SEQ ID NO 58; 55pp; English.  
 CC The invention relates to identifying an agent that modulates  
 CC intracellular calcium comprises monitoring the effects of the agent on  
 CC store-operated calcium entry comprising contacting one or more test cells  
 CC or their portion comprising one or more proteins that is (are) at least  
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or  
 CC CG5842 over at least about 40% of the encoded protein (and that provides  
 CC for store-operated calcium entry with a test agent), where the portion of  
 CC the cell comprises the proteins, monitoring the effect(s) of the test  
 CC compound on store-operated calcium entry and identifying a test agent as  
 CC an agent if it has an effect on store-operated calcium entry. Also  
 CC included are a method of modulating store-operated calcium entry  
 CC (comprising modulating the level of, expression of, activity of or  
 CC molecular interactions of a protein in a cell that has altered store-  
 CC operated calcium entry, where the protein is at least about 35%  
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842  
 CC over at least about 40% of the encoded protein and that provides for  
 CC store-operated calcium entry, and where store-operated calcium transport  
 CC into the cell is modulated) and a method of identifying a molecule that  
 CC provides for store-operated calcium entry (comprising identifying a  
 CC molecule that interacts with the protein mentioned above, thus,  
 CC identifying molecules involved in modulating store-operated calcium  
 CC entry. The protein does not contain the contiguous sequences appearing as  
 CC ADI81644 and ADI81645. The proteins are selected from ion transport  
 CC proteins. The method is useful in modulating, or in identifying agents  
 CC that modulate, intracellular calcium. These may be used in treating  
 CC diseases associated with calcium dysregulation, such as neurodegenerative  
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory  
 CC diseases (e.g. aschma or rheumatoid arthritis), cancer, liver diseases  
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.  
 CC glomerulonephritis). The present sequence represents an identified  
 CC homologue of one of the two above mentioned drosophila proteins.  
 CC  
 CC Sequence 871 AA:  
 SO  
 Query Match 99.2%; Score 3829; DB 8; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 361 NLEAVLNNDGLSPLMMAAKTGKIGI FQHTIRREVTDETRHLSKFKDMAVGPVYSSLYD 420  
 QY 421 LSSLDTCGEASVTEILVYNSKIENRHEMLAVEPINELLDCKMRKFGAVSFYINVSYL 480  
 DB 421 LSSLDTCGEASVTEILVYNSKIENRHEMLAVEPINELLDCKMRKFGAVSFYINVSYL 480  
 QY 481 AMVIFTLTAAYOPLBEGTPPYRRTVDYRLAESEVITLFTGLVFFFTNIDLPKKRPGV 540  
 DB 481 AMVIFTLTAAYOPLBEGTPPYRRTVDYRLAESEVITLFTGLVFFFTNIDLPKKRPGV 540  
 QY 541 NSLFDGSPQLVFIYSVLVYSAALYAGIBAYLAWMPALVGMNNALYFRGLKLTG 600  
 DB 541 NSLFDGSPQLVFIYSVLVYSAALYAGIBAYLAWMPALVGMNNALYFRGLKLTG 600  
 QY 601 TYSIMOKILFKDLFFRLVYLLFMIGASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 DB 601 TYSIMOKILFKDLFFRLVYLLFMIGASALVSLNPCANMKVCNEDQNTCTVPTPSC 660  
 QY 661 RDEETSTFLDPEFKLTIGMDLEMSSTKYPVVFIIIVTYIILFVLLNMLALMGE 720  
 DB 661 RDEETSTFLDPEFKLTIGMDLEMSSTKYPVVFIIIVTYIILFVLLNMLALMGE 720  
 QY 721 TVGQVSKSKHIMKLTQ 736  
 DB 721 TVGQVSKSKHIMKLTQ 736  
 RESULT 13  
 ABB98197  
 ID ABB98197 standard; protein; 871 AA.  
 AC ABB98197;  
 DT 12-DEC-2002 (first entry)  
 XX Human VR-OAC amino acid sequence.  
 KW Human: VR-OAC: vanilloid receptor-related osmotically activated channel;  
 KW anti-HIV; antistematic; immunomodulator; cerebroprotective;  
 KW antidiabetic; antifertility; auditory; antipruritic; dermatological;  
 KW antipsoriatic; antiallergic; anorectic; neuroprotective;  
 KW ophthalmological; nootropic; cytosstatic; nephroprotective; hypotensive;  
 KW analgesic; mechanoreception; mechanosensation; hearing disorder; HIV;  
 KW Human immunodeficiency virus; obesity; vertigo; motion sickness;  
 KW neurological disorder; ataxia; male infertility; immune dysfunction;  
 KW diabetes mellitus; chronic obstructive lung disorder; bronchial asthma;  
 KW sexual dysfunction; blindness; skin disorder; psoriasis; kidney disease;  
 KW arterial hypertension; pain syndrome; Alzheimer's disease; dementia;  
 KW hydrocephalus; alopecia; baldness; cancer.  
 OS Homo sapiens.  
 PN WO200259152-A2.  
 XX  
 PD 01-AUG-2002.  
 XX 26-OCT-2001; 2001WO-US050539.  
 XX 26-OCT-2000; 2000US-0243568P.  
 PR 25-OCT-2001; 2001US-00243568.  
 XX (UYRQ ) UNITV ROCKEFELLER.  
 XX  
 XX Liedtke W, Heller S, Hudspeth AJ, Friedman JW;  
 DR WPI: 2002-599762/64.  
 DR N-PSDB; ABQ79489.  
 PT Modulating mechanoreception or mechanosensation, for diagnosing,  
 PT preventing or treating e.g. hearing disorders, HIV or obesity, comprises  
 PT administering a vanilloid receptor-related osmotically activated channel  
 PT polypeptide.



XX Claim 2; Fig 2; 154pp; English.

XX The invention relates to modulating mechanoreception/mechanosensation in

CC a mammal by administering a vanilloid receptor-related osmotically

CC activated channel (VR-OAC) polypeptide, its active fragments or portions,

CC or by introducing a nucleic acid vector capable of expressing the VR-OAC

CC polypeptide. The method of the invention is useful for modulating

CC mechanoreception or mechanosensation, for diagnosing, preventing or

CC treating e.g. hearing disorders, Human Immunodeficiency virus (HIV),

CC obesity, vertigo of labyrinthine origin including motion sickness,

CC neurological disorders including ataxia, male infertility, immune

CC dysfunction, diabetes mellitus, chronic obstructive lung disorder,

CC bronchial asthma, sexual dysfunction, blindness due to corneal or retinal

CC causes, or skin disorders including psoriasis. Other conditions include

CC arterial hypertension, kidney diseases, pain syndromes, Alzheimer's

CC disease and other dementias, hydrocephalus, alopecia, baldness and

CC cancer. The VR-OAC may be used in detecting or assessing osmotic and

CC mechanical stimuli, or as the facilitating component in translating an

CC osmotic or mechanical stimulus in nano-technological, biosensor or

CC biobiotic devices. The current sequence represents the amino acid

CC sequence of human VR-OAC as determined from HEK293 cells. NOTE: The

CC inventors indicate the presence of further VR-OAC polypeptides other than

CC those given in records AB98197-8. However, no sequence information

CC regarding these polypeptides which are referred to as SEQ ID's 5, 6, 7, 8

CC and 9 is given

XX

XX Sequence 871 AA.

Query Match 99.2%; Score 3828; DB 5; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANDSEPPRAGPGEVATLPGDESGTGGGAFFPLSLANLFGEGDGLSPADASRAGP 60  
 DB 1 MANDSEPPRAGPGEVATLPGDESGTGGGAFFPLSLANLFGEGDGLSPADASRAGP 60  
 QY 61 GDGRPNRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAPMDSLFDTGYRHSDDN 120  
 DB 61 GDGRPNRMKFGQAFKRGVNPIDLESTLYESSVVPKPKAPMDSLFDTGYRHSDDN 120  
 QY 121 KRMKRTIIEKOPQSPKAPAPPPILKYFNRPILFDIVSRGSTADLDGLPLTLTHKKRL 180  
 DB 121 KRMKRTIIEKOPQSPKAPAPPPILKYFNRPILFDIVSRGSTADLDGLPLTLTHKKRL 180  
 QY 181 TDEFRERPSRGKTLCPALNLSNGRNDTIPVLDIERTGNMKEFINSFRDLYYRGQT 240  
 DB 181 TDEFRERPSRGKTLCPALNLSNGRNDTIPVLDIERTGNMKEFINSFRDLYYRGQT 240  
 QY 241 ALHAIERCKHAYVELLVAQCADVHAQARGFQPKDGGYFYFGEPLSLIACTNPHI 300  
 DB 241 ALHAIERCKHAYVELLVAQCADVHAQARGFQPKDGGYFYFGEPLSLIACTNPHI 300  
 QY 301 VNYITENPHKADNRQDSRGNTVLAHALVAADNTRENTKVTYMDLLKCARLPDS 360  
 DB 301 VNYITENPHKADNRQDSRGNTVLAHALVAADNTRENTKVTYMDLLKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPILMAAKTKIGIFQHIIRREVDETRHLSRFKDMAYGPVSSLYD 420  
 DB 361 NLEAVLNNDGLSPILMAAKTKIGIFQHIIRREVDETRHLSRFKDMAYGPVSSLYD 420  
 QY 421 LSSIDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLDKMKKRGAVSYINVSYL 480  
 DB 421 LSSIDTCGEASVLEIIVYNSKIENRHEMLAVEPINELLDKMKKRGAVSYINVSYL 480  
 QY 481 AMVFTLTAYOPLGPTPPYRTVDYLRLAGVITLFTGVLPFTNLIKLEMKKCGV 540  
 DB 481 AMVFTLTAYOPLGPTPPYRTVDYLRLAGVITLFTGVLPFTNLIKLEMKKCGV 540  
 QY 541 NSLFDIGSFOLLFYFYSVLVIVSAAVLAGIETAYAVVAFVIGMNAALFYTRGLKLG 600  
 DB 541 NSLFDIGSFOLLFYFYSVLVIVSAAVLAGIETAYAVVAFVIGMNAALFYTRGLKLG 600

QY 601 TYSIMIOKILFKDLERFELLVILLFMIGYASALVSLINPCANMKVCNEDQNTCTVPTPSC 660  
 DB 601 TYSIMIOKILFKDLERFELLVILLFMIGYASALVSLINPCANMKVCNEDQNTCTVPTPSC 660  
 QY 661 RSEFTSTLIDLFKLTICMGDEMLSTKPYVFIILVYTIILFVLLNMLLMGE 720  
 DB 661 RSEFTSTLIDLFKLTICMGDEMLSTKPYVFIILVYTIILFVLLNMLLMGE 720  
 QY 721 TWGVSKESKHWKLQ 736  
 DB 721 TWGVSKESKHWKLQ 736

RESULT 14  
 AD181590  
 ID AD181590 standard; protein; 871 AA.  
 XX  
 AC AD181590;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DX Human vanilloid receptor-related channel protein #1.  
 XX  
 KW Human; calcium entry modulator; CD4536; CG5842; intracellular calcium;  
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;  
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;  
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004009537-A1.  
 PD 15-JAN-2004.  
 XX  
 PE 13-JAN-2003; 2003US-00342844.  
 XX  
 PR 11-JAN-2002; 2002US-0347459P.  
 PR 02-AUG-2002; 2002US-0401171P.  
 PR 20-AUG-2002; 2002US-0405678P.  
 XX  
 PA (ROOS/) ROOS J.  
 PA (STAU/) STAUDERMAN K.  
 PA (VELI/) VELICELEBI G.  
 PI Roos J, Stauderman K, Velicelebi G;  
 XX  
 DR MPI: 2004-090465/09.  
 DR N-PSDB; AD181589.  
 XX  
 PT Identifying an agent that modulates intracellular calcium levels, useful  
 PT for treating diseases associated with calcium dysregulation (e.g.  
 PT cancer), comprises monitoring the effects of the agent on store-operated  
 PT calcium entry.  
 XX  
 PS Disclosure; SEQ ID NO 60; 55pp; English.

XX The invention relates to identifying an agent that modulates

CC intracellular calcium comprising monitoring the effects of the agent on

CC store-operated calcium entry comprising contacting one or more test cells

CC or their portion comprising one or more proteins that is (are) at least

CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or

CC CG5842 over at least about 40% of the encoded protein (and that provides

CC for store-operated calcium entry with a test agent), where the portion of

CC the cell comprises the proteins, monitoring the effect(s) of the test

CC compound on store-operated calcium entry and identifying a test agent as

CC an agent if it has an effect on store-operated calcium entry. Also

CC (comprising modulating the level of, expression of, activity of or

CC molecular interactions of a protein in a cell that has altered store-

CC operated calcium entry, where the protein is at least about 35%

CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842

CC over at least about 40% of the encoded protein and that provides for

CC store-operated calcium entry, and where store-operated calcium transport

CC into the cell is modulated) and a method of identifying a molecule that  
 CC provides for store-operated calcium entry (comprising identifying a  
 CC molecule that interacts with the protein mentioned above, thus,  
 CC identifying molecules involved in modulating store-operated calcium  
 CC entry. The protein does not contain the contiguous sequences appearing as  
 CC AD181644 and AD181645. The proteins are selected from ion transport  
 CC proteins. The method is useful in modulating, or in identifying agents  
 CC that modulate, intracellular calcium. These may be used in treating  
 CC diseases associated with calcium dysregulation, such as neurodegenerative  
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory  
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases  
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.  
 CC glomerulonephritis). The present sequence represents an identified  
 CC homologue of one of the two above mentioned drosophila proteins.  
 XX

Sequence 871 AA;

Query Match 99.2%; Score 3828; DB 8; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFBGEGSLSPSPADARRPAGP 60
DB 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFBGEGSLSPSPADARRPAGP 60
QY 61 GGRPNLMMKFOGAFKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120
DB 61 GGRPNLMMKFOGAFKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120
QY 121 KMRKKLIEKOPSPAPAPOPPPILKVNRRPILFDIVSRGSTADLDGLPFLTHKKRL 180
DB 121 KMRKKLIEKOPSPAPAPOPPPILKVNRRPILFDIVSRGSTADLDGLPFLTHKKRL 180
QY 181 TDEEREPESTGTCTPKALINLSNGNDTIPVLLDIAETGMMREINSPPDIYRGQT 240
DB 181 TDEEREPESTGTCTPKALINLSNGNDTIPVLLDIAETGMMREINSPPDIYRGQT 240
QY 241 AHHIAIERCKAYVELVAQADVAHQARGFQPDGEGYFYGELPLSLAATNQPHI 300
DB 241 AHHIAIERCKAYVELVAQADVAHQARGFQPDGEGYFYGELPLSLAATNQPHI 300
QY 301 VVYLLENPKKADNRQDSRGNTVLAVALADNTRNTKPTKYATDILLKCARLPDS 360
DB 301 VVYLLENPKKADNRQDSRGNTVLAVALADNTRNTKPTKYATDILLKCARLPDS 360
QY 361 NLEAVLNNDGSLPLMAAATGKIGIFQHTIRREVTDEDETRHLSRKFCKMAVGYVSSLYD 420
DB 361 NLEAVLNNDGSLPLMAAATGKIGIFQHTIRREVTDEDETRHLSRKFCKMAVGYVSSLYD 420
QY 421 LSSLDTCGEBASVLEILVYNSKIENRHEMLAVEPINEILDRDKRRKFGAVSFYINVSYLIC 480
DB 421 LSSLDTCGEBASVLEILVYNSKIENRHEMLAVEPINEILDRDKRRKFGAVSFYINVSYLIC 480
QY 481 AMVITLTAAYOPLGTPPYPRRTVDYKRLAGEVITLFTGLPFFTNIKDLFMKKCPGV 540
DB 481 AMVITLTAAYOPLGTPPYPRRTVDYKRLAGEVITLFTGLPFFTNIKDLFMKKCPGV 540
QY 541 NSLFIIDGSGFOLLFYFYSVLVISAALYLAGIAYLAWVAFVLCMMNALYTRGLKLTG 600
DB 541 NSLFIIDGSGFOLLFYFYSVLVISAALYLAGIAYLAWVAFVLCMMNALYTRGLKLTG 600
QY 601 TYSIMIQILFEDLFRLLVYLLEMIIGYASALVSLNFCANMKVCNEDQNTCTVYTESC 660
DB 601 TYSIMIQILFEDLFRLLVYLLEMIIGYASALVSLNFCANMKVCNEDQNTCTVYTESC 660
QY 661 RDSEFFSTFLDLFLTLTGMDLEMLSTKYPVVITLILVYITLFTVLLMLIALMGE 720
DB 661 RDSEFFSTFLDLFLTLTGMDLEMLSTKYPVVITLILVYITLFTVLLMLIALMGE 720
QY 721 TVGQVSKSKHIMKLO 736
DB 721 TVGQVSKSKHIMKLO 736

```

# RESULT 15

AD808372 ID AD808372 standard; protein; 970 AA.

AC AD808372;

DT 29-JAN-2004 (first entry)

DE Novel protein (useful for identifying genetic disorders) #527.

XX novel gene; novel protein; tissue marker; molecular weight marker;

KW chromosome marker; genetic disorder.

XX Unidentified.

OS WO2003054152-A2.

PN 03-JUL-2003.

PD 10-DEC-2002; 2002WO-US039555.

PF 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.

PR 12-APR-2002; 2002US-0372615P.

PR 22-APR-2002; 2002US-00128558.

PR 24-APR-2002; 2002US-0376045P.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh W, Xue AJ, Wehrman T, Wang G, Zhou P, Dymnac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

PI WPI; 2003-569235/53.

DR N-PSDB; AD807461.

PT New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

PS Claim 20; SEQ ID NO 1438; 1177bp; English.

XX The invention comprises the amino acid and coding sequences of novel

XX proteins. The DNA and protein sequences of the invention are useful as:

XX markers for tissues in which the corresponding protein is preferentially

XX expressed; as molecular weight markers on gels; as chromosome markers or

XX tags; to identify chromosomes or to map related gene positions; and to

XX compare with endogenous DNA sequences in patients to identify potential

XX genetic disorders. The present amino acid sequence represents a protein

XX of the invention.

XX

Sequence 970 AA;

Query Match 99.2%; Score 3828; DB 7; Length 970;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFBGEGSLSPSPADARRPAGP 60
DB 1 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFBGEGSLSPSPADARRPAGP 159
QY 100 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFBGEGSLSPSPADARRPAGP 159
DB 100 MADSSGPRAGPGEVAELPDGSGTGGGAFFPLSLANLFBGEGSLSPSPADARRPAGP 159
QY 61 GGRPNLMMKFOGAFKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120
DB 61 GGRPNLMMKFOGAFKGVNPIDLESTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 219
QY 121 KMRKKLIEKOPSPAPAPOPPPILKVNRRPILFDIVSRGSTADLDGLPFLTHKKRL 180
DB 121 KMRKKLIEKOPSPAPAPOPPPILKVNRRPILFDIVSRGSTADLDGLPFLTHKKRL 279

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QY 181 TDEEFREPSTGKTCLPKALINLSNGRNDIIPVLLDIAERTGNMREFINSPPFDIYYRGQT 240
    |||||
Db 280 TDEEFREPSTGKTCLPKALINLSNGRNDIIPVLLDIAERTGNMREFINSPPFDIYYRGQT 339
    |||||
QY 241 ALHIAIERCKKHYVELLVAGADVAHQAGRPQPKDBGGYFYFGELPLSLAAGTNPBH 300
    |||||
Db 340 ALHIAIERCKKHYVELLVAGADVAHQAGRPQPKDBGGYFYFGELPLSLAAGTNPBH 399
    |||||
QY 301 VNYLTENPKKADMRKODSRGNTVLAVALADNTRENTKFTYKMDLLILKCARLFPDS 360
    |||||
Db 400 VNYLTENPKKADMRKODSRGNTVLAVALADNTRENTKFTYKMDLLILKCARLFPDS 459
    |||||
QY 361 NLEAVLNDGSLPMMAAKTGKIGIFQHIIRREVTDSDTRHLSRKFKDWAAGPYSSLYD 420
    |||||
Db 460 NLEAVLNDGSLPMMAAKTGKIGIFQHIIRREVTDSDTRHLSRKFKDWAAGPYSSLYD 519
    |||||
QY 421 LSSLDTGGEASVLELIVYNSKTIENHHEMLAVEPINELLRDKKRRKGAVSFYINVSYL 480
    |||||
Db 520 LSSLDTGGEASVLELIVYNSKTIENHHEMLAVEPINELLRDKKRRKGAVSFYINVSYL 579
    |||||
QY 481 AMVIFTLTAAYOPLBEGTPPYRYRTVDYRLAGEVITLFTGVLPFFTNIKDLFMKKCPGV 540
    |||||
Db 580 AMVIFTLTAAYOPLBEGTPPYRYRTVDYRLAGEVITLFTGVLPFFTNIKDLFMKKCPGV 639
    |||||
QY 541 NSLFFIDGSFQLYFYISVLIYSALYLAGIEAYLAVMPFALVGMNNALYFTRGKLTG 600
    |||||
Db 640 NSLFFIDGSFQLYFYISVLIYSALYLAGIEAYLAVMPFALVGMNNALYFTRGKLTG 699
    |||||
QY 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPGANMKVCNEDQNCVPTYPSC 660
    |||||
Db 700 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPGANMKVCNEDQNCVPTYPSC 759
    |||||
QY 661 RDSETFSTFLDLFKLTIKGDLEMLSTKYPVFIIILVTYIILTFVLLNNMLALMGE 720
    |||||
Db 760 RDSETFSTFLDLFKLTIKGDLEMLSTKYPVFIIILVTYIILTFVLLNNMLALMGE 819
    |||||
QY 721 TVGQVSKSKHMKLQ 736
    |||||
Db 820 TVGQVSKSKHMKLQ 835
    |||||
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Search completed: December 2, 2004, 22:23:18  
Job time : 168 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 22:20:35 ; Search time 41 Seconds  
(Without alignments)  
1200.194 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858  
Sequence: 1 MADSSGPRAGGEVAELPG.....GVSKSKHIMWLQSGRRRL 742

Scoring table: BIOSUM62  
Gapco 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	4	US-09-500-123-12 Sequence 12, Appl
2	3823	99.1	871	4	US-09-500-123-7 Sequence 7, Appl
3	3470	89.9	811	4	US-09-500-123-9 Sequence 9, Appl
4	1604.5	41.6	843	3	US-09-235-451-25 Sequence 25, Appl
5	1604.5	41.6	843	4	US-09-978-303-25 Sequence 25, Appl
6	1579.5	40.9	838	4	US-09-235-451-2 Sequence 2, Appl
7	1579.5	40.9	838	4	US-09-132-316-3 Sequence 3, Appl
8	1579.5	40.9	838	4	US-09-667-422-9 Sequence 9, Appl
9	1579.5	40.9	838	4	US-09-978-303-2 Sequence 2, Appl
10	1557.5	40.4	839	3	US-09-197-636-2 Sequence 2, Appl
11	1556.5	40.3	839	3	US-09-197-636-8 Sequence 8, Appl
12	1556.5	40.3	839	3	US-09-235-451-34 Sequence 34, Appl
13	1556.5	40.3	839	4	US-09-978-303-4 Sequence 4, Appl
14	1555.5	40.3	839	4	US-09-533-220A-2 Sequence 2, Appl
15	1552.5	40.2	839	3	US-09-197-636-4 Sequence 4, Appl
16	1551.5	40.2	839	4	US-09-667-422-4 Sequence 4, Appl
17	1324	34.3	761	3	US-09-235-451-4 Sequence 4, Appl
18	1324	34.3	761	4	US-09-978-303-4 Sequence 4, Appl
19	1306	33.9	889	4	US-09-132-316-2 Sequence 2, Appl
20	1298.5	33.7	764	3	US-09-235-451-36 Sequence 36, Appl
21	1298.5	33.7	764	4	US-09-978-303-36 Sequence 36, Appl
22	1071	27.8	511	4	US-09-667-422-5 Sequence 5, Appl
23	777	20.1	727	4	US-09-235-451-23 Sequence 23, Appl
24	777	20.1	727	4	US-09-978-303-23 Sequence 23, Appl
25	733	19.0	727	4	US-09-350-457A-4 Sequence 4, Appl
26	724.5	18.8	725	4	US-09-350-457A-2 Sequence 2, Appl
27	548.5	14.2	279	4	US-09-149-476-500 Sequence 500, Appl

28	227	5.9	71	3	US-09-235-451-14 Sequence 14, Appl
29	227	5.9	71	4	US-09-978-303-14 Sequence 14, Appl
30	221.5	5.7	1709	4	US-09-392-812A-6 Sequence 6, Appl
31	210	5.4	1619	4	US-09-392-812A-4 Sequence 4, Appl
32	180	4.7	1704	4	US-09-392-812A-2 Sequence 2, Appl
33	172	4.5	1095	3	US-09-112-096-15 Sequence 15, Appl
34	172	4.5	1095	4	US-09-636-215-778 Sequence 778, App
35	172	4.5	1095	4	US-09-685-166A-778 Sequence 778, App
36	172	4.5	1095	4	US-09-679-426-778 Sequence 778, App
37	169	4.4	1095	4	US-09-636-215-780 Sequence 780, App
38	169	4.4	1095	4	US-09-685-166A-780 Sequence 780, App
39	169	4.4	1095	4	US-09-679-426-780 Sequence 780, App
40	155	4.0	1503	4	US-09-600-087-2 Sequence 2, Appl
41	146	3.8	57	3	US-09-235-451-15 Sequence 15, Appl
42	146	3.8	57	4	US-09-978-303-15 Sequence 15, Appl
43	137	3.6	316	4	US-09-461-325-378 Sequence 378, App
44	137	3.6	316	4	US-10-012-542-378 Sequence 378, App
45	137	3.6	316	4	US-10-115-123-378 Sequence 378, App

ALIGNMENTS

RESULT 1  
US-09-500-123-12  
; Sequence 12, Application US/09500123  
; Patent No. 6455278  
; GENERAL INFORMATION:  
; APPLICANT: Dublin, Adrienne E  
; APPLICANT: Huvar, Arne  
; APPLICANT: Erlander, Mark G  
; APPLICANT: Glass, Charles A  
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor  
; FILE REFERENCE: Human VR3 receptors  
; CURRENT APPLICATION NUMBER: US/09/500,123  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 742  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-500-123-12

Query Match	Best Local Similarity	Score	DB 4	Length	742
Matches	742	Conservative	0	Mismatches	0
Indels	0	Gaps	0		
QY	1	MADSSGPRAGGEVAELPGDESGTGGRAFLSSIANLFEEDGSLSPSPADASPAPG	60		
DB	1	MADSSGPRAGGEVAELPGDESGTGGRAFLSSIANLFEEDGSLSPSPADASPAPG	60		
QY	61	GGGRNLNWKFOGAERKGVNPIDLESTLYESSVVPKPKAPMDLFDYGYRRHSSDN	120		
DB	61	GGGRNLNWKFOGAERKGVNPIDLESTLYESSVVPKPKAPMDLFDYGYRRHSSDN	120		
QY	121	KMRKRTIEKQPSKAPAPPPPLIKVNNRIIDYRSRGTADIGLPLTHKKRL	180		
DB	121	KMRKRTIEKQPSKAPAPPPPLIKVNNRIIDYRSRGTADIGLPLTHKKRL	180		
QY	181	TDEPRESTGTCTPKALLNLSNGRNDTIPVLLIABRTGMREFINSPPFDIYRGQT	240		
DB	181	TDEPRESTGTCTPKALLNLSNGRNDTIPVLLIABRTGMREFINSPPFDIYRGQT	240		
QY	241	ALHIAIERCKHYVELVAQADVAQAGRFQPKDGGYFFGELPLSLAAGTNPRI	300		
DB	241	ALHIAIERCKHYVELVAQADVAQAGRFQPKDGGYFFGELPLSLAAGTNPRI	300		
QY	301	VNYLTENHKKADMRQDSRGNTVLAVALADNTRENTKPYTKYDILLKCAALFPDS	360		
DB	301	VNYLTENHKKADMRQDSRGNTVLAVALADNTRENTKPYTKYDILLKCAALFPDS	360		

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QY 361 NLEAVLNNDGSLPIMMAAKTGKIGIFQHIIRREVTDDETRHLSRKEKDMAYGCVSSLYD 420
DB 361 NLEAVLNNDGSLPIMMAAKTGKIGIFQHIIRREVTDDETRHLSRKEKDMAYGCVSSLYD 420
QY 421 LSLDTCGEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
DB 421 LSLDTCGEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
QY 481 AMVIFLTLAYOPLBETPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
DB 481 AMVIFLTLAYOPLBETPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
QY 541 NSLFDGSPQLLYFIYSVLYSALYLAGIEAYLAWMPALVGMNNALYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFIYSVLYSALYLAGIEAYLAWMPALVGMNNALYFTRGLKLTG 600
QY 601 TYSIMTQKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMTQKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
QY 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNNLIALMGE 720
DB 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNNLIALMGE 720
QY 721 TVGVSKESKHIMKLGSRRL 742
DB 721 TVGVSKESKHIMKLGSRRL 742

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RESULT 2  
US-09-500-123-7  
Sequence 7, Application US/09500123  
Patent No. 6455278

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; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne B
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-500-123-7

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Query Match 99.1%; Score 3823; DB 4; Length 871;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MADSSBGRAPGGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
DB 1 MADSSBGRAPGGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
QY 61 GDGSPNLRMKQGAFRKGVNPNPILBESTLYESSVVPKKAAMDLSFDYGTVRHSSDN 120
DB 61 GDGSPNLRMKQGAFRKGVNPNPILBESTLYESSVVPKKAAMDLSFDYGTVRHSSDN 120
QY 121 KRMWKIIIEKOPQSPKAPAPPPPLIKVFNPIILFDIYSGSTADLDGLLPFLTHKKRL 180
DB 121 KRMWKIIIEKOPQSPKAPAPPPPLIKVFNPIILFDIYSGSTADLDGLLPFLTHKKRL 180
QY 181 TDEFRPSTGKTLCPKALNLSNGRNDTIPVLLDIARTGNMGEFINSPPRDIIYRGOT 240
DB 181 TDEFRPSTGKTLCPKALNLSNGRNDTIPVLLDIARTGNMGEFINSPPRDIIYRGOT 240
QY 241 ALHAIERRCHGYVELLAQADVAHQARGFPOPKDGGYIFRSELPLSLAAGCTNOPI 300
DB 241 ALHAIERRCHGYVELLAQADVAHQARGFPOPKDGGYIFRSELPLSLAAGCTNOPI 300

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DB 241 ALHAIERRCHGYVELLAQADVAHQARGFPOPKDGGYIFRSELPLSLAAGCTNOPI 300
QY 301 VNYLTENPKKADMRKODSRGNTVLAVALADNTRENTKVTYKMYDLILKCARLPDS 360
DB 301 VNYLTENPKKADMRKODSRGNTVLAVALADNTRENTKVTYKMYDLILKCARLPDS 360
QY 361 NLEAVLNNDGSLPIMMAAKTGKIGIFQHIIRREVTDDETRHLSRKEKDMAYGCVSSLYD 420
DB 361 NLEAVLNNDGSLPIMMAAKTGKIGIFQHIIRREVTDDETRHLSRKEKDMAYGCVSSLYD 420
QY 421 LSLDTCGEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
DB 421 LSLDTCGEASVLEILVYNSKIENHMLAVEPINELLRDKRKKGAVSFYINVSYL 480
QY 481 AMVIFLTLAYOPLBETPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
DB 481 AMVIFLTLAYOPLBETPPPYRTVDYRLAGEVITLFTGVLPFTNIDLPKCKPGV 540
QY 541 NSLFDGSPQLLYFIYSVLYSALYLAGIEAYLAWMPALVGMNNALYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFIYSVLYSALYLAGIEAYLAWMPALVGMNNALYFTRGLKLTG 600
QY 601 TYSIMTQKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMTQKILFKDLFFRLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
QY 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNNLIALMGE 720
DB 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFTVLLNNLIALMGE 720
QY 721 TVGVSKESKHIMKLG 736
DB 721 TVGVSKESKHIMKLG 736

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RESULT 3  
US-09-500-123-9  
Sequence 9, Application US/09500123  
Patent No. 6455278

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; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne B
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-500-123-9

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Query Match 89.9%; Score 3470; DB 4; Length 811;  
Best Local Similarity 91.7%; Pred. No. 0;  
Matches 675; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

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QY 1 MADSSBGRAPGGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
DB 1 MADSSBGRAPGGEVAVELPGDESGTGGEARPLSLANLFGEDGSLSPSPADASRPAGP 60
QY 61 GDGSPNLRMKQGAFRKGVNPNPILBESTLYESSVVPKKAAMDLSFDYGTVRHSSDN 120
DB 61 GDGSPNLRMKQGAFRKGVNPNPILBESTLYESSVVPKKAAMDLSFDYGTVRHSSDN 120
QY 121 KRMWKIIIEKOPQSPKAPAPPPPLIKVFNPIILFDIYSGSTADLDGLLPFLTHKKRL 180
DB 121 KRMWKIIIEKOPQSPKAPAPPPPLIKVFNPIILFDIYSGSTADLDGLLPFLTHKKRL 180
QY 181 TDEFRPSTGKTLCPKALNLSNGRNDTIPVLLDIARTGNMGEFINSPPRDIIYRGOT 240
DB 181 TDEFRPSTGKTLCPKALNLSNGRNDTIPVLLDIARTGNMGEFINSPPRDIIYRGOT 240
QY 241 ALHAIERRCHGYVELLAQADVAHQARGFPOPKDGGYIFRSELPLSLAAGCTNOPI 300
DB 241 ALHAIERRCHGYVELLAQADVAHQARGFPOPKDGGYIFRSELPLSLAAGCTNOPI 300

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```

QY 181 THEPEPEPSTGKTCLEKALLINTSNGNDTTPVLDDIAERGNMREFINSFPDIYRGQT 240
Db 181 TDEEPEPEPSTGKTCLEKALLINTSNGNDTTPVLDDIAERGNMREFINSFPDIYRGQT 240
QY 241 ALHIAIERCKHVELLVQAQADVMAQARFPQPODEGGYEFKGEIPLSLAQTQPHI 300
Db 241 ALHIAIERCKHVELLVQAQADVMAQARFPQPODEGGYEFKGEIPLSLAQTQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLAALVALADNTRENTKFTYKMYDLLLKKARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAALVALADNTRENTKFTYKMYDLLLKKARLPDS 360
QY 361 NLEAVLNNGSPLIMMAKTGKIGIFOHIIIREVTEDTRHSRKEKDMAYGEVSSLYD 420
Db 361 NLEAVLNNDGSLPIMMAAKTG----- 381
QY 421 LSSLDTGCEASVLEILVYNSKIENHEMLAVEPINELLRDKWRKEGAVSFYINVSYYC 480
Db 382 -----KIENHEMLAVEPINELLRDKWRKEGAVSFYINVSYYC 420
QY 481 AMVITFTLLAYYQPLEGTPPYPRRTYVDYLRAGEVITLFTGVLFPEFTNKKDLFMKKCPGV 540
Db 421 AMVITFTLLAYYQPLEGTPPYPRRTYVDYLRAGEVITLFTGVLFPTNKKDLFMKKCPGV 480
QY 541 NSLIFDSFQOLLYFTYSVLVYISAAIYLAGIEAYAVMPEALVLGMMNALYFTRGKLTG 600
Db 481 NSLIFDSFQOLLYFTYSVLVYISAAIYLAGIEAYAVMPEALVLGMMNALYFTRGKLTG 540
QY 601 TYSIMIQKILFKDLFRFLVLVLYLFMIGASALVSLNIPCANMKVCNEODTNCVTPYBSC 660
Db 541 TYSIMIQKILFRDLFRFLVLVLYLFMIGASALVSLNIPCANMKVCNEODTNCVTPYBSC 600
QY 661 RDSEFTSFLLDLFKLITIGMDILEMSTKYVVEFIILVTYIILFTVYLLNMLTALMGE 720
Db 601 RDSEFTSFLLDLFKLITIGMDILEMSTKYVVEFIILVTYIILFTVYLLNMLTALMGE 660
QY 721 TVGQVSKSKSIHWKQ 736
Db 661 TVGQVSKSKSIHWKQ 676

```

```

RESULT 4
US-09-235-451-25
: Sequence 25, Application US/09235451
: GENERAL INFORMATION:
: APPLICANT: Julius, David J.
: APPLICANT: Caterina, Michael J.
: APPLICANT: Brake, Anthony J.
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
: TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: 9076/084CIP
: CURRENT APPLICATION NUMBER: US/09/235,451
: CURRENT FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/072,151
: PRIOR FILING DATE: 1998-01-22
: PRIOR APPLICATION NUMBER: 08/915,451
: PRIOR FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 25
: LENGTH: 843
: TYPE: PRT
: ORGANISM: chicken
: US-09-235-451-25

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Query Match      41.6%  Score 1604.5  DB 3  Length 843;
Best Local Similarity 47.5%  Pred. No. 1.2e+14;
Matches 343; Conservative 128; Mismatches 184; Indels 67; Gaps 18;

Qy 41 EGEDEGSSPADSRFRAGGPDGKRNLMKQGAFRKVEVFIDLLSTLY--ESSVYPG 98
      |||||
Db 27 DGEDSAL--ETAD-----NLOGTF--SKVQPSKSNIFARRRFRFWG 64

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QY 99 ----PKKAPMDSFDY-----GTYHSSDNNKRMKRIIEKOP---QSPKAPAPORPELIL 146
Db 65 DDDCKMAMPDSYQMDHLMAPSVYKHNANKERKHKHLKSTDSITGCSSEA-----F 116
QY 147 KVPNRPILFEDIVSRGSTADLDLPELTLTHKKRLTDEEFREPSPTGKTCLEKALINLSNGR 206
Db 117 KEYDRRRIJFDAVARSGSTODDLLLYLNTLKHLTDEFEKEPEPTGKTLCKAMLNLDGK 176
QY 207 NDTIVLLDIAARTGMMREFTISPRDIIYRQGTALHIAIERCKAYVELLYAQADVHA 266
Db 177 NDTIPELLDIAKTLGKLEFEVAEYTDNYKQOTALHIAIERNMMLIVKLYQNGADVHA 236
QY 267 QARGFEPOP-KDEGGFYFGELEPLSLAACCTNOPIHYNUTENDHKKADMRDROSRGTVL 325
Db 237 RACGEFFRKIKKPG-FYFGELEPLSLAACCTNOLCIKPLENPYQADIAAESMGMMVL 295
QY 326 HALVALIANTRENTKFTVKMYDLMLLKCARLFPDSNLEAVLNDGSLPMLMAKTKIGI 385
Db 296 HTLVEIANTKONTKEFVKMYNNIILGKINPILKELELTNKKKGLTPLTAAKTKIGI 355
QY 386 FOHITRREVTEDTETHLSRKFKDMAYGPVYSSLYDLSIDTQGEBAVLEIIVYNSKIN 445
Db 356 FAYILRRRIKQPECHLSRKFTEMAYGPHSSLYDLSIDTC-EKXSVLEIITAYSETPN 414
QY 446 RHEMLIAYPIMELLRDKMRKFGANSFYINNVSYLCAMVITLTAYYQPLE-GRPEPYX- 502
Db 415 RHEMLIAYPILKRLLODKMDRFVKHLYFNFEPYALHISLTLYAAYRPQKGDKPPFAG 474
QY 503 RTTYDYLELAGSVTLFTGVLEFFENIKDLEPKKQGVNSLIDGSPOLLIFYISLVIV 562
Db 475 HSTGEHYRVTIEIISVLOGLYFFEPGIC-YFQRRPSLKTLLIVDSYSEVLFPVHSLILS 533
QY 563 SAALYIAGIABAYLAVMVEPALVIGMMNALYFTRGLTLGTYSIMIOKLEFKDLFRFLYVL 622
Db 534 SVVLYFCQGEHYVASMVESLALGVANMLYTRGFGQMGYISYIMAKMILRDCRPFYVL 593
QY 623 LEMIGVASAYSLINPCANMKVCNEDQ-TNCTVPIYPSGRDSEYTSY-----FLDLIF 674
Db 594 VFLIGFSTAVVTLIED-----DNEGQDINS-EYARCSHKKRKRSTYSNLYYTLEIF 645
QY 675 KLITIGMDLEMLSTTKPVVFIILLVYIIITLVYIILMLIYALMGEYVGOVSKESKHIWK 734
Db 646 KFTIGMGDLBETENYRFRKSVFVILLYLVILYIITLIMLITAKMEITYSKIAQESKSIWK 705
QY 735 LQ 736
Db 706 LQ 707

```

```

RESULT 5
US-09-978-303-25
; Sequence 25, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; FILE REFERENCE: UCL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/691,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25

```

LENGTH: 843  
 TYPE: PRF  
 ORGANISM: chicken  
 US-09-978-303-25

Query Match  
 Best Local Similarity 47.5%; Pred. No. 1.2e-143;  
 Matches 343; Conservative 128; Mismatches 184; Indels 67; Gaps 18;

QY 41 EHGDSLSPPADASPAGDGRPLRKFGAFKGVNPIIDLESTLY--ESSVPG 98  
 DB 27 DEBDSAL--ETAD-----NLQSTF-----SNKQPSKSNIFARRGFVNG 64  
 QY 99 ----PKKAPMDSLFDY-----GTYRHSSDNKMRKKIIEKQP---QSPAPAPQPPILL 146  
 DB 65 DCDKMAFMDSFQOMHLAPSVIKFHANERGLKHLSTDSITGCSERA-----F 116  
 QY 147 KVENREPLDIYVRSSTADIDGLPLTHKKQLTDEEPREPSTGKTCPLKALLINSGR 206  
 DB 117 KEVDRRIRFDVAVARGSTKOLDLILYINRTLKHLLTDEFEKPEPSTGKTCPLKAMLNHDGK 176  
 QY 207 NDPIPLVLDIAEKTGMNREFINSPRDIYRSGTALHAIERCKHYVELLVOGADVHA 266  
 DB 177 NDPIPLVLDIAEKTGMNREFINSPRDIYRSGTALHAIERCKHYVELLVOGADVHA 226  
 QY 267 QARGREFOP-KDEGGEYFEGELPLSLAAGTNPVHIVYLTENPHKADMRRODSRGNTVL 325  
 DB 237 RAGEFFRKIKKRG-FYFGEPLSLAAGTNPVHIVYLTENPHKADMRRODSRGNTVL 295  
 QY 326 HALVALADNTRENTKPVTKYDILLKCARLPDPSNLEAVLANDGLSPLMAAKTGICG 385  
 DB 296 HTLVIAADNTKNTKFTVKYNNILILGAKINPLIKLEELTNKKGLPLPLAATGKIGI 355  
 QY 386 FOHIIREVDEDETRHLSRKKDMAGVYVSYSLYDLSLDTGCEASVLEIVNSKIE 445  
 DB 356 FAYILREIADPECRHLSRKKDMAGVYVSYSLYDLSLDTGCEASVLEIVNSKIE 414  
 QY 446 RHEMLAVEPINELLDKMRKGAVSFYINVSYLCAVNIPLTAVYQPLR--GTPPYV- 502  
 DB 415 RHEMLAVEPINELLDKMRKGAVSFYINVSYLCAVNIPLTAVYQPLR--GTPPYV- 474  
 QY 503 RTIVDYLRLAGEVITLFTGVLPFTNIDKLFMKKCPGVNSLFDISQQLYFYSVIV 562  
 DB 475 HSTGEYFRVYGEILSYVGLVFFFRGIGQ-YVQRRPRLKTLIVDSYSEVLEFVNSLILLS 533  
 QY 563 SAALYIAGIEYIYAVMFAVILVGMNALLYFRGKLGITYSIMIOKILFQDLFFLLVYL 622  
 DB 534 SVVLYFCQDELIVASWVFSIALGMANMLYTRGFQOMGIYSVMAKILRDLCRFMEVYL 593  
 QY 623 LFMIGYASALVSLNPCANMKVCNEDQ-TNCTVPTYPSCRDSETFST-----FLIDLF 674  
 DB 594 VFLIGFSYAVVLTLED-----DNEGQDTNS--EYARCSHTKRGRTSYNSLYTCELEF 645  
 QY 675 KLITGMGDELMSTKYPVFTIILVYIITFVLLNMLIALMGETVGVSKSKHILWK 734  
 DB 646 KFTIGMGDELETFENYRKSVEFVILVYIITFVLLNMLIALMGETVSKIAQSKSIWK 705  
 QY 735 LQ 736  
 DB 706 LQ 707

RESULT 6  
 US-09-235-451-2  
 Sequence 2, Application US/09235451

GENERAL INFORMATION:  
 APPLICANT: Julius, David J.  
 APPLICANT: Caterina, Michael J.  
 APPLICANT: Brake, Anthony J.  
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
 TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
 TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
 FILE REFERENCE: 9076/084CIP

CURRENT APPLICATION NUMBER: US/09/235,451  
 CURRENT FILING DATE: 1999-01-22  
 PRIOR APPLICATION NUMBER: 60/072,151  
 PRIOR FILING DATE: 1998-01-22  
 PRIOR APPLICATION NUMBER: 08/915,461  
 PRIOR FILING DATE: 1997-08-20  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 838  
 TYPE: PRF  
 ORGANISM: R. rattus  
 US-09-235-451-2

Query Match  
 Best Local Similarity 40.9%; Score 1579.5; DB 3; Length 838;  
 Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

QY 16 AELRGDSGTGGE-----AFPLSLANLPEGEDGSLSPADDA 54  
 DB 5 ASDSESSSPQENSCLDPPDRDNCCKPPYKPHILFTTRSKTRLF-GKQDSSEASPLDC 63  
 QY 55 SRPAGDGRPMLRMKFGAFKGVN-PIIDLESTLYSESVVGPKKAPMDSLFDYGY 113  
 DB 64 PYREG-----GLASCPILTVSVL---TIQREGDGP-----ASV 94  
 QY 114 RHHSNKRMRKKIIEKQPOSPPAPAPQPPILLKVENRPIEDIVRGSTADIDGLPL 173  
 DB 95 RPSQDS-----VSAGEKRP--RLYDRRSIFPAVAVQSNQCELESLLPL 136  
 QY 174 LTHKKQLTDEEPREPSTGKTCPLKALLINSGRNDITPVLLDAERTGNRREINSPFRD 233  
 DB 137 ORSKRLTDEEPREPSTGKTCPLKAMLNHNGNDITALLDVARKTDLSKQFVNASYTD 196  
 QY 234 IYRGQTALHAIERCKHYVELLVOGADVHAQARGFPOPEDEGYFFFGELPLSLAA 293  
 DB 197 SYKKGQTALHAIERCKHYVELLVOGADVHAQARGFPOPEDEGYFFFGELPLSLAA 256  
 QY 294 CTNQHPIVNYLTENPHKADMRRODSRGNTVHALVALADNTRENTKPVTKYDILLK 353  
 DB 257 CTNQHPIVNYLTENPHKADMRRODSRGNTVHALVALADNTRENTKPVTKYDILLK 316  
 QY 354 ARLEPDSNLEAVLNNDQSLPMAAKTGICGFOHIIREVDEDETRHLSRKKDMAGV 413  
 DB 317 AKHPLTKLEITTRKGLTPALAASSGKIGVLAIIQRIHBECHLSKFTEMAYGP 376  
 QY 414 VYSLYDLSLDTGCEASVLEILVY-NSKIERHEMLAVEPINELLDKMRKGAVSFY 472  
 DB 377 VHSLSYDLSLDTGCEASVLEILVY-NSKIERHEMLAVEPINELLDKMRKGAVSFY 435  
 QY 473 INVVSYLCAVNIPLTAVYQPLEGTPPYRTTY-DYLRLAGEVITLFTGVLPFTNIXD 531  
 DB 436 FNFVYCIYMIIFTPAAVYRVEBGLPPYKKNVGDYFRVYGEILTSVSGVYFFFRGIGQ- 494  
 QY 532 LFMKKCPGVNSLFDISQQLYFYSVIVYSAALYIAGIEYIYAVMFAVILVGMNALLY 591  
 DB 495 YFQRRPRLKTLIVDSYSEVLEFVNSLILLS 554  
 QY 592 FTRGKLTGYYSIMIOKILFQDLFFLLNMLIALMGETVGVSKSKHILWK 651  
 DB 555 YTRGFQOMGIYVAVMIEKMLRDLCRFMEVYLVFFGFSTAVVTLI-----EDGKN 604  
 QY 652 CTVP---TYPSCRDS-----ETFTPLDLPFKLITGMGDELMSTKYPVFTIIL 699  
 DB 605 NSLPWSTPHKCRGACKCPGANSVNSLYST-CLIEFPKFTIGMGDELETFENYFKAIVFTILL 663  
 QY 700 VTYIILFTVLLNMLIALMGETVGVSKSKHILWK 736  
 DB 664 LAYILVYIILNMLIALMGETVKNIAQSKSIWK 700

RESULT 7  
 US-09-132-316-3



```

; Sequence 3, Application US/09132316B
; Patent No. 6444440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1468.1110000
; CURRENT APPLICATION NUMBER: US/09/132.316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 838
; TYPE: PRN
; ORGANISM: Rattus norvegicus
; US-09-132-316-3

```

```

Query Match      40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

```

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16 ABLPGDESGTGGG-----AFPLSLANLFEEDGSLSPSPADA 54
5 ASLDSSESESPQENSCLDPDRDPNCKPPVPHFTTRSRTRLF-GKGDSEASPLDC 63
55 SRPAGGDDRPVLRMKFGQAFKGVN-PIDLLESTLVSSVPGKAPMOSLFRYGY 113
64 PYERG-----GLASCPITVSSVL-----TIQREGDP-----ASV 94
114 RHSSDNKRWKRIIEKOPQSPKAPAPQPPILKVFNPRLPFIIVSRGSTADLDGLPFL 173
95 RSSQDS-----VSAGEKP--RLYDRSIFDVAQNSCQLESILPFL 136
174 LTHKRLTDEEREPSTGTCTCPKALLNSNGRNTPIVLDIAERTGNMREFINSPPD 233
137 QRSKRLTDESEKDEPTGKTCILKMLNHNQNDTIALLDVARKTDSLKQFVNASYD 196
234 IYRGQTALHIAIERCKHYVELVAQADVAHQAARGFPQKDGSGYYPGELPISLAA 293
197 SYKQGTALHIAIERKNTLVTLVENGADVAAGDFKTKGRPGFYFGLPLSLAA 256
234 CTNPHIVNYLTENPHKADMRDGRGNTVLAHVAIADNTRENTKFTKYADLLILKC 353
257 CTNGLAIYKFLQNSWQPADISARDSVGNTVLHALVEADNTVDNTKFTSYNNEILLIG 316
354 ARLPDSNLEAVLNDGSLPMAAKTGIGIFOHITREVTDETRHLSRKFQWANGP 413
317 AKLHPTLKLEITRNKGLTPPLAASSGKIGVLAIVLQREIHPECRHLSRKFTEWANGP 376
414 VYSSLYDSSLDTCGEASVLEIIVY-NSKIENRHEMLAVBPINELDKMKKFGAVSGY 472
377 VHSSTLYDSSLDTC- EKNSVLEIVAYSSSETRNDMLVBPINELDKMKRPFYKRIFY 435
473 INVSYLCAMVIFLTAYQPLEGTPPYRYTTV-DYRLAGEVITLFTGYLFFPTNICK 531
436 FNEFYCYLMIFLTAAYRYRVEGPPYTKANTVEDYFRVYSEILSVSGGVFFFRGIC- 494
532 LPMKCKPGVNSLFDGSQLFYISVLTIVSAALYAGIEAVLAVMVFALVGMNNALY 591
495 YFLGRPSIKSLFVDSYEILFFVQSLFVLVSVLVYFSQRKEYVASVTFSLAMGMTNLY 554
592 FTGKGLTGYSIMOKLFLFDLRFLLVYLFLMIGVASALVSLNPPCANMKVCEDQTN 651
555 YIRGQMGITAVMIEKMLRDLCKRPMFYIVLFLGFSIAVVTLL-----EDKN 604
652 CTVP---TYPSCRDS-----ETFSFLDLFLFKLTIGMGDLMLSLTKYPVVFIIL 699
605 NSLPEWSTPHKCRGACGCKRGNSVNSLYST-CLFLPKFTIGMGDLLEFTEINYPKAVFIIL 663

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Qy 700 VTYIILFVLLANMLALMGRTVGOVSKSHIKWLO 736
Db 664 LAVVILTYILLNMLALMGEIVYKIAQESKNIMKLO 700

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## RESULT 8

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US-09-667-422-9
; Sequence 9, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRN
; ORGANISM: Rattus sp.
; PUBLICATION INFORMATION:
; AUTHORS: Caterina, Michael J.
; AUTHORS: Schumacher, Mark A.
; AUTHORS: Tomioka, Makoto
; AUTHORS: Rosen, Tobias A.
; TITLE: The capsaicin receptor: a heat-activated ion channel in
; JOURNAL: Nature
; VOLUME: 389
; PAGES: 816-824
; DATE: 1997
; US-09-667-422-9

```

```

Query Match      40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

```

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16 ABLPGDESGTGGG-----AFPLSLANLFEEDGSLSPSPADA 54
5 ASLDSSESESPQENSCLDPDRDPNCKPPVPHFTTRSRTRLF-GKGDSEASPLDC 63
55 SRPAGGDDRPVLRMKFGQAFKGVN-PIDLLESTLVSSVPGKAPMOSLFRYGY 113
64 PYERG-----GLASCPITVSSVL-----TIQREGDP-----ASV 94
114 RHSSDNKRWKRIIEKOPQSPKAPAPQPPILKVFNPRLPFIIVSRGSTADLDGLPFL 173
95 RSSQDS-----VSAGEKP--RLYDRSIFDVAQNSCQLESILPFL 136
174 LTHKRLTDEEREPSTGTCTCPKALLNSNGRNTPIVLDIAERTGNMREFINSPPD 233
137 QRSKRLTDESEKDEPTGKTCILKMLNHNQNDTIALLDVARKTDSLKQFVNASYD 196
234 IYRGQTALHIAIERCKHYVELVAQADVAHQAARGFPQKDGSGYYPGELPISLAA 293
197 SYKQGTALHIAIERKNTLVTLVENGADVAAGDFKTKGRPGFYFGLPLSLAA 256
234 CTNPHIVNYLTENPHKADMRDGRGNTVLAHVAIADNTRENTKFTKYADLLILKC 353
257 CTNGLAIYKFLQNSWQPADISARDSVGNTVLHALVEADNTVDNTKFTSYNNEILLIG 316
354 ARLPDSNLEAVLNDGSLPMAAKTGIGIFOHITREVTDETRHLSRKFQWANGP 413
317 AKLHPTLKLEITRNKGLTPPLAASSGKIGVLAIVLQREIHPECRHLSRKFTEWANGP 376
414 VYSSLYDSSLDTCGEASVLEIIVY-NSKIENRHEMLAVBPINELDKMKKFGAVSGY 472
377 VHSSTLYDSSLDTC- EKNSVLEIVAYSSSETRNDMLVBPINELDKMKRPFYKRIFY 435
473 INVSYLCAMVIFLTAYQPLEGTPPYRYTTV-DYRLAGEVITLFTGYLFFPTNICK 531

```

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Db 436 FNFVYCLMIIFTAAAYRPEVGLPPYKLKNTVGDYFRTGELLVSGGVFFFRGIG- 494
Qy 532 LFMKCPGNLSLPIFDSFOLLFYIVYSAALYAGIEMVAVLAVLGMNALLY 591
Db 495 YFLORRPSLKSIFVDSYSILFFVQSLFVLVSVLYFSQRKEVAVSMVSLAMGWTNMLY 554
Qy 592 FTRGLKLTGYSTIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPMCANMKVCNEDQTN 651
Db 555 YTRGFQOMGIYAVMIEMKILRDLCRFMFVYLVLFQFSTAVVTLI-----EDGKX 604
Qy 652 CTVP---TYPSCRDS-----ETFSFLDLFLKLTIGMDLEMLSTKYPVVFIIIL 699
Db 605 NSLPMESTHKCRGSAKCPGNNSLYST-CELEFFTLIGMDLEFFTENYDFRAVFIILL 663
Qy 700 VTYIILTFVILLMLTALMGETVGOVSKSKHIMKIQ 736
Db 664 LAVIILTYILLMLTALMGETVNAKIAOSKNIMKIQ 700

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## RESULT 9

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US-09-978-303-2
; Sequence 2, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsacin receptor and capsacin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UOAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
US-09-978-303-2

```

Query Match 40.9%; Score 1579.5; DB 4; Length 838;

Best Local Similarity 44.6%; Pred. No. 3e-141;

Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

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Qy 16 AELPDSGSGTPEG-----APPLSLANLFRGDSLSPPADA 54
Db 5 ASDLSSESSESPQNSCLDPPDRDPNCKPPVYKHITTSRTLLF-GKGSSEASLDC 63
Qy 55 SRPAGPDGSRNLMKFGAERKGVN-PIDLSTLYESSVDFPKAPMDSLFYGYTY 113
Db 64 PYERG-----GLASCPITVSSVL-----TIORPDGP-----ASV 94
Qy 114 RHSSDNKKRKKIIEKOPQSPKAPAPQRPILVFNRPILFDIVSGSTADLGLPFL 173
Db 95 RPSQDS-----VSAGEKPP-RLYDRSRIFDVAQSNCELSLPL 136
Qy 174 LTHKKRLTDEEFREPSGTCTCPKALNLSNGRNDTIFVLIDIAERTGNMREPTNSPRD 233
Db 137 QRSKRLTDSFQPEPTKTCILKRLMNLHNGQDITALLDVAARKDSLQGFVNASYTD 196
Qy 234 IYVGGTALHAIERCKHYVELLVAQADYHAQGRFFQPKDBGYFYGEHPLSLAA 293
Db 197 SYVGGTALHAIERRNMTLVTLVYENGADYQAANGDFPKTKGRPGFYGEHPLSLAA 256
Qy 294 CTNQHPIVNYLTENPHKADMRQDSRGNTVLAHALADTRNTKFTVTGYDILLK 353

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Db 257 CTNQLAIYKELLQNSQNPADISARDSVGNVLAHALVEADNTVDNKTFTSMNELLIG 316
Qy 354 ARLFPDSNLKAVLINDGSLPMLMAATKGIQFQHIIRREVTDETRHLSRKFQWAGP 413
Db 317 AKLHPLKLEITNKRGLTPALMASSCKIGVLAYLQREIHBPGRHLSRKFTEWAGP 376
Qy 414 VYSSLYDLSLDTGCEHAAVLEIIVY-NKINRHEMLAVEPNNELARKKWRFGAVSFY 472
Db 377 VSSSLDLSLCIDTC-EKNSLVLAIVSSSETPRKMDLVEPLNRLQDNMRDFVGRITY 435
Qy 473 INVSYLCAMVIFTLTAVYQPLEGTPPYRYRTV-DYLRAGEVITLFTGVLEFFTNIKD 531
Db 436 FNFVYCLMIIFTAAAYRPEVGLPPYKLKNTVGDYFRTGELLVSGGVFFFRGIG- 494
Qy 532 LFMKCPGNLSLPIFDSFOLLFYIVYSAALYAGIEMVAVLAVLGMNALLY 591
Db 495 YFLORRPSLKSIFVDSYSILFFVQSLFVLVSVLYFSQRKEVAVSMVSLAMGWTNMLY 554
Qy 592 FTRGLKLTGYSTIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPMCANMKVCNEDQTN 651
Db 555 YTRGFQOMGIYAVMIEMKILRDLCRFMFVYLVLFQFSTAVVTLI-----EDGKX 604
Qy 652 CTVP---TYPSCRDS-----ETFSFLDLFLKLTIGMDLEMLSTKYPVVFIIIL 699
Db 605 NSLPMESTHKCRGSAKCPGNNSLYST-CELEFFTLIGMDLEFFTENYDFRAVFIILL 663
Qy 700 VTYIILTFVILLMLTALMGETVGOVSKSKHIMKIQ 736
Db 664 LAVIILTYILLMLTALMGETVNAKIAOSKNIMKIQ 700

```

## RESULT 10

```

US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
; APPLICANT: DICKWORTH, DAVID
; APPLICANT: HAYES, PHILIP
; APPLICANT: MEADOWS, HELEN
; APPLICANT: DAVIS, JOHN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,636
; FILING DATE: 23-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9805137.8
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: UK 9815791.0
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: UK 9819278.4
; FILING DATE: 03-SEP-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

```

! INFORMATION FOR SEQ ID NO: 2:

! SEQUENCE CHARACTERISTICS:  
! LENGTH: 839 amino acids  
! TYPE: amino acid  
! STRANDEDNESS: single  
! TOPOLOGY: linear  
! MOLECULE TYPE: protein  
! US-09-197-636-2

Query Match 40.4%; Score 1557.5; DB 3; Length 839;  
Best Local Similarity 44.5%; Pred. No. 3,7e-139;  
Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

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QY 49 PSPADASRPAGGDDGRPNL-----RMKFGQ-----AFKGVNPIIDLES--TLYESV 95
DB 22 PDLIDGDNRPAPKPOLSTAKSRTLFGKGDSEAFVDCPHEBGLDSCPTTVSPV 81
QY 96 V-----PGPKAPMDSLFYGYTRHSSDNKMKKIIKOPSPKAPAPPPPIIKVF 149
DB 82 ITIQRPDGGPTGARL-----LSQDSVAASTEKTLRLY 113
QY 150 NRPIIDIVSRGSTADLDGLPPLTHKKRLTDEFRREPSTGKCLPKALNLSGRNDT 209
DB 114 DRSIFEAVAQNCCODESLLEFLQSKKHLTDNEFKDPTGKTLKAMLNLDGQNTT 173
QY 210 IPIVLDIAERTGNMREFINSPPFDIYRGQTALHAIERRCKHYVELVAOGADVAQAR 269
DB 174 IPIVLEIARQDLSLKELVNASYDYSYKQGTALHAIERRNMAVTLVLENGADVQAAAH 233
QY 270 GRFPQKDEGGYFYFGEIPLSLAAGTNOPIHIVYLTENPHKADMRQDSRGNTVLAHV 329
DB 234 GDFEKKTKRGPGYFGEIPLSLAAGTNOPIHIVYLTENPHKADMRQDSRGNTVLAHV 293
QY 330 AIADNTRENTKFTKMYDILLKCARLPDSNLEAVLNNDGSLPMAAATGKIGIFOHI 389
DB 294 EVADNTADNTKFTKMYDILLKCARLPDSNLEAVLNNDGSLPMAAATGKIGIFOHI 353
QY 390 IRRVTDDETRHLRKPKMAVGPVYSLSYDLSLDTGCEBASVLEILVY-NSKIENRHE 448
DB 354 IRRVTDDETRHLRKPKMAVGPVYSLSYDLSLDTGCEBASVLEILVY-NSKIENRHE 412
QY 449 MLAVEPILNELLKDKRKPKAVSFYINVSILCAMVFTLTAYIQPLEGPPYPRRTVDY 508
DB 413 MLAVEPILNELLKDKRKPKAVSFYINVSILCAMVFTLTAYIQPLEGPPYPRRTVDY 472
QY 509 IRLAGEVITLFTGVLEFFTNIKDLPMKCPGVNSLPIFDSPOLVLYFVSALVLA 568
DB 473 FRYTGEIILSVLGIVYFFFRGIGQ-YFLQRPSPSKTILFVDSYSEKLEFLOSLFMLATVLYF 531
QY 569 AGIEAYLAVMVFALVIGMNNALYTRGKLITGYSIMIQILFKDLFRELLVYLLFMIGY 628
DB 532 SHIKKEYVAVSMVFSLALGWTNMLYTRGFGQWGIYAVMIEKMLIRDLCRMFFIYIFLEGF 591
QY 629 ASALVSLNPKANMKVNCNEDQNCVPTV-----PSCRDSER-----PSTFLDLDFK 675
DB 552 STAAVTLA-----EDGKNDLSESTSHRRRGAPCRPDSDYNSLYST-CLIELEFK 640
QY 676 LTIIGADLEMLSTKYPVVFILLVYIILFVLLINMLIAMEGTGVSSEKSHIWM 735
DB 641 FTIGGDLLEFTEYVFKAVFILLVYIILFVLLINMLIAMEGTGVSSEKSHIWM 700
QY 736 Q 736
DB 701 Q 701

```

RESULT 11

US-09-197-636-8  
! Sequence 8, Application US/09197636  
! Patent No. 6239267  
! GENERAL INFORMATION:  
! APPLICANT: DUCKWORTH, DAVID  
! APPLICANT: HAYES, PHILIP

```

! APPLICANT: MEADOWS, HELEN
! APPLICANT: DAVIS, JOHN
! TITLE OF INVENTION: NOVEL COMPOUNDS
! NUMBER OF SEQUENCES: 8
! CORRESPONDENCE ADDRESS:
! ADDRESSEE: Ratner & Prestia
! STREET: P.O. Box 980
! CITY: Valley Forge
! STATE: PA
! COUNTRY: US
! ZIP: 19482-0980
! COMPUTER READABLE FORM:
! MEDIUM TYPE: Diskette
! COMPUTER: IBM Compatible
! OPERATING SYSTEM: DOS
! SOFTWARE: FastSeq for Windows Version 2.0
! CURRENT APPLICATION DATA:
! APPLICATION NUMBER: US/09/197,636
! FILING DATE: 23-NOV-1998
! CLASSIFICATION:
! PRIOR APPLICATION DATA:
! APPLICATION NUMBER: UK 9805137.8
! FILING DATE: 12-MAR-1998
! APPLICATION NUMBER: UK 9815791.0
! FILING DATE: 21-JUL-1998
! APPLICATION NUMBER: UK 9819278.4
! FILING DATE: 03-SEP-1998
! ATTORNEY/AGENT INFORMATION:
! NAME: Prestia, Paul F
! REGISTRATION NUMBER: 23,031
! REFERENCE/DOCKET NUMBER: GP-30075
! TELECOMMUNICATION INFORMATION:
! TELEPHONE: 601-407-0700
! TELEFAX: 610-407-0701
! TELEX: 846169
! INFORMATION FOR SEQ ID NO: 8:
! SEQUENCE CHARACTERISTICS:
! LENGTH: 839 amino acids
! TYPE: amino acid
! STRANDEDNESS: single
! TOPOLOGY: linear
! MOLECULE TYPE: protein
! US-09-197-636-8

Query Match 40.3%; Score 1556.5; DB 3; Length 839;
Best Local Similarity 44.5%; Pred. No. 4,7e-139;
Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

QY 49 PSPADASRPAGGDDGRPNL-----RMKFGQ-----AFKGVNPIIDLES--TLYESV 95
DB 22 PDLIDGDNRPAPKPOLSTAKSRTLFGKGDSEAFVDCPHEBGLDSCPTTVSPV 81
QY 96 V-----PGPKAPMDSLFYGYTRHSSDNKMKKIIKOPSPKAPAPPPPIIKVF 149
DB 82 ITIQRPDGGPTGARL-----LSQDSVAASTEKTLRLY 113
QY 150 NRPIIDIVSRGSTADLDGLPPLTHKKRLTDEFRREPSTGKCLPKALNLSGRNDT 209
DB 114 DRSIFEAVAQNCCODESLLEFLQSKKHLTDNEFKDPTGKTLKAMLNLDGQNTT 173
QY 210 IPIVLDIAERTGNMREFINSPPFDIYRGQTALHAIERRCKHYVELVAOGADVAQAR 269
DB 174 IPIVLEIARQDLSLKELVNASYDYSYKQGTALHAIERRNMAVTLVLENGADVQAAAH 233
QY 270 GRFPQKDEGGYFYFGEIPLSLAAGTNOPIHIVYLTENPHKADMRQDSRGNTVLAHV 329
DB 234 GDFEKKTKRGPGYFGEIPLSLAAGTNOPIHIVYLTENPHKADMRQDSRGNTVLAHV 293
QY 330 AIADNTRENTKFTKMYDILLKCARLPDSNLEAVLNNDGSLPMAAATGKIGIFOHI 389
DB 294 EVADNTADNTKFTKMYDILLKCARLPDSNLEAVLNNDGSLPMAAATGKIGIFOHI 353
QY 390 IRRVTDDETRHLRKPKMAVGPVYSLSYDLSLDTGCEBASVLEILVY-NSKIENRHE 448

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Db		354	LÖRITQBECHLSRKFTBMAVGPBHSYIDSCIDTC-EKNSVLEAVIAYSSSEPPNRND	412
QY		449	MLAVEPINELIDYRKFTGAVSFYINVSYLCAWIFPILTAIYQLEGGPPFPRTYDY	508
Db		413	MLAVEPINRLLIADKKDRFVKRI FYENFPLVYCIYMIIFWMAAYRPVDGJLPPKMEKXTGY	472
QY		509	LRAGEVITLFTGYLFEFFPTNFKDLPKKCPGNSLFIJGSFOLAYEYSVLIVASATYL	568
Db		473	FRVWGEIISVJGYYFFFRGJO-YLQGRPSMKTLFVDSYSMLFPLQSLFMALATVLF	531
QY		569	AGIEBAYIAVMYFATVLGMMNALYETRGKLTJSTYSIMIOKILFKDLFRLLIYLLFMIGY	628
Db		532	SHLEKYVASWFSIALGWTNMLYYTRGGEQOMGIYAVMIKMLIRDJCRMFYVYVFLFQP	591
QY		629	ASALVSYILNPANMKVNCEDQNTCVPTV-----PSCRDSER-----FSTFLDLDFK	675
Db		592	STAVATLL-----EDGNDSLPSESTSHRRMRGRCRPPDSSYNSLYST-CLELRK	640
QY		676	LTIGNGDEMLSTKYPVVFIIILVTYIIILFVLLIMLIALMGETVGVSSKSKHIMWL	735
Db		641	FTIGNGDLEFENYDFKAVFIILLIAYVILFYIILLIMLIALMGETVGNKIADSKNIWKL	700
QY		736	Q 736	
Db		701	Q 701	

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RESULT 12
US-09-235-451-34
; Sequence 34, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235.451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 839
; TYPE: prf
; ORGANISM: Homo sapiens
US-09-235-451-34

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Query Match	40.3%	Score 1556.5	DB 3	Length 839			
Best Local Similarity	44.5%	Pred. No. 4.7e-139					
Matches	321	Conservative 138	Mismatches 188	Indels 74			
				Gaps 12			
Qy	49	PSPADASRPAAGGDRGPNL----	RMKTQG----	APRKGVNPFIDLLS--	TYIESV	95	
Db	22	PPLLDGDEPSRPPAKPOLSTAKSRTRL	LQKGDSEAFVVD	CPNHEGELDSCPTITV	SPV	81	
Qy	96	V-----	PPKKAPMDSLFDYGYNNHSSDNKRWK	KII	IKGQSPKAPAPQEPILKVF	149	
Db	82	ITTQRGGDPFGKRL-----			LQDSVAAS	TEXTIRLY 113	
Qy	150	NRPILFDIYSRGS	TADLDGLPFL	LTHKRL	LDEEFREB	STGTC	LPKALLNSGRNDT 209
Db	114	DRSIFEAVANN	CCDLSEILLFL	QSKGKL	LDNEKQ	DETKTCL	KAMLLIHGQNTT 173
Qy	210	ITVLDIARTGNM	EFINS	PRDIYYRG	QTALHT	AIERCGHY	VELLVAOGADVYACAR 269
Db	174	IPLLLEIAQOTS	LKELVN	ASTDYKQ	GTALHIL	IERNNAL	ITVLLVYENGADVQAAAH 233

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QY 270 GRFOPRDEBGEYFKEGLPISLACTNPHVNYTEPHKADRRDSDSRNTYLAHV 329
Db 234 GDFPKTKRKRGPFYFGLPISLACTNOLGIVKFLLONSMOTADLSARDVSQNTYLAHV 293
QY 330 AIDNTRBENTKVTQWYDLLLKCARLFPDSNLEAVLNNDGLSPMLMAAKTKIGIPOHI 389
Db 294 EVAENTADNTEKFTVSMYNEIILIGAKHPITLKEBLTNKKGMTPALAAGTKIGIVLAVI 353
QY 390 IRREVTEQDTHLSRKPKDMAYGPFYSLSYDLSLDTGCEASVLEIIVY-NSKIENRHE 448
Db 354 LORIOPECHLSRKPTFEMAYGVSHTYDLSCTDTC-EKNSVLEVIAYSSSEPNRRD 412
QY 449 MLAVERNELLDRKMRKGAVSFYINAVSYLCAMVIFLLTAYOQLEGTPPRYPTTYD 508
Db 413 MLVEPNERLLQDKMDRPFVKRIIFYENFLVYCIYMIIFMAAYRRVVDGIAPPEKMRKGTGY 472
QY 509 LRAGEVLTFTGYLFFPTNIKDLFEKKCPGVNSFLIDGSPOLAFIYSVLIYSAALV 568
Db 473 FRVGEISLTVAGVYFFFRGJIO-YLQDRPSKTIKTFVDSYSMLFFLOSLFMALATVLYX 531
QY 569 AGIEAYLAWVPALVIGMNAUYFTRGILKTGYTSIMOKILFKDLFRLLVYLFLMICY 628
Db 532 SHLKEYVASWFSLAGWTNNMLYYTRGCOQMGIVAWMEIKMLIRDCRFMYVAVFLFGP 591
QY 629 ASALVSLINPCANMKVCNEDQNCVPVY-----PSCRDSER-----FSTFLDLDFK 675
Db 592 STAVATTL-----EDGKNSDLPBSRSTHMRKGRACRPPDSYNSLYST-CLDLRK 640
QY 676 LTIIGDLEMLDSTKYPVFIIILVYIIILFVLLINMLIALMGETVOGVSKESKIHWL 735
Db 641 FTIGGDLFEFTENYDFKAVFIILLAYVILFIYLLINMLIALMGETVNKIAQESKNIMWL 700
QY 736 Q 736
Db 701 Q 701

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1      RESULT 13
2      US-09-978-303-34
3      ; Sequence 34, Application US/09978303
4      ; Patent No. 6790629
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Julius, David J.
7      ; APPLICANT: Caterina, Michael J.
8      ; APPLICANT: Brake, Anthony J.
9      ; TITLE OF INVENTION: Nucleic acid sequences encoding
10     ; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
11     ; TITLE OF INVENTION: polypeptides and uses thereof
12     ; FILE REFERENCE: UCAL084CON
13     ; CURRENT APPLICATION NUMBER: US/09/978, 303
14     ; CURRENT FILING DATE: 2001-10-15
15     ; PRIOR APPLICATION NUMBER: 09/235,451
16     ; PRIOR FILING DATE: 1999-01-22
17     ; PRIOR APPLICATION NUMBER: 60/072,151
18     ; PRIOR FILING DATE: 1998-01-22
19     ; PRIOR APPLICATION NUMBER: 08/915,461
20     ; PRIOR FILING DATE: 1997-08-20
21     ; NUMBER OF SEQ ID NOS: 48
22     ; SOFTWARE: FaalSeq for Windows Version 4.0
23     ; SEQ ID NO 34
24     ; LENGTH: 839
25     ; TYPE: prt
26     ; ORGANISM: Homo sapiens
27     ; US-09-978-303-34

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Query Match	40.3%	Score 1556.5	DB 4	Length 839	
Local Similarity	44.5%	Pred. No. 4.7e-139			
Best Local					
Matches 311	Conservative 138	Mismatches 188	Indels 74	Gaps 12	
QY	49	PSPADASRAGCGDGRPT	-----RMKQG-----	AFKGVNPIDTLES	95
		-----	-----	-----	
DB	22	PPLDLDPPNSPPKPFQSLTKSKTRLLFGKSDSEAFVYDCEPHHEGGLDSCPTITVSPV			81

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QY 96 V-----PGPKKAPMDSLPDYGYTRHSSDNKRWKRIIEKOPSPAPAPQPPILKVF 149
DB 82 ITTORPDGPTGARL-----LSQSVAASTKRTLR 113
QY 150 NRPLPIVSRGSTADIDGLLPILLTHKKRLTDEEPREPTGKTCPLKALINLSNGNDT 209
DB 114 DRSIFBAVAONNODLESLLFLQSKKHLTNEFPDPTGKTCCLKAMLNLDGQNTT 173
QY 210 IPLLDAERTGNMREPIINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 269
DB 174 IPLLDAERTGNMREPIINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 233
QY 270 GREFQPDGEGYFPGELPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 329
DB 234 GDEFFKTKGRPGFYFGLPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 293
QY 330 AIDNRENTKFTYKMYDLILKCARLPDSNLEAVLNNDGLSPIMAAATGKIGFOHT 389
DB 294 EVADNTADNTKFTYKMYDLILKCARLPDSNLEAVLNNDGLSPIMAAATGKIGFOHT 353
QY 390 IREEVDEDTRLSRKFKDMAYGVPYSSLYDLSLDTGCEASVLEILVY-NSKIENRHE 448
DB 354 LOREIOBECRHLSRKFKTEWAVGPHVSSLYDLSLDTGCEASVLEILVY-NSKIENRHE 412
QY 449 MAVEPINELLRDKMRKFGAVSFYINVSYLCAWITFTLTAAYQPLEGTPPYRYRTVDY 508
DB 413 MLVEPINELLRDKMRKFGAVSFYINVSYLCAWITFTLTAAYQPLEGTPPYRYRTVDY 472
QY 509 LRLAGEVITLFTGVLFPEFTNICKLFEMKCCPGVNSLFDISGFOLLYFYSVLVISAALYL 568
DB 473 FRTYGLISLVGVSVEFFRGIQ-YFLQRRBSMKTLEFVDSSEMLFLOSLFMLATVLYLF 531
QY 569 AGIEAVLAVWVFLVGMNNAIYTRGLKLTGYTSIMIQIKLFKDFRPLVLYLLPMIGY 628
DB 532 SHKEVYASVWVFLVGMNNAIYTRGLKLTGYTSIMIQIKLFKDFRPLVLYLLPMIGY 591
QY 629 ASALVSLNPCAMKVCNEDQNTCTVPTY-----PSCRDSCT-----FSTFLDLFX 675
DB 592 STAVVTLI-----EDGKNDSLPSSESTSHRWGAPACRPDSSVNSLYST-CLELFX 640
QY 676 LITGMGDLMLSTKYPVFIILVYIILTFVLLNMLIALMGFTVGVGSKESKRIWKL 735
DB 641 FTIGMDLEFTENYDKAVFIILVYIILTFVLLNMLIALMGFTVGVGSKESKRIWKL 700
QY 736 Q 736
DB 701 Q 701

```

RESULT 14  
 US-09-533-220A-2  
 ; Sequence 2, Application US/09533220A  
 ; Patent No. 6406908  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McIntyre, Peter  
 ; APPLICANT: James, Iain Frazer  
 ; TITLE OF INVENTION: Human Vanilloid Receptor  
 ; FILE REFERENCE: 4-30875A  
 ; CURRENT APPLICATION NUMBER: US/09/533,220A  
 ; PRIOR FILING DATE: 2000-03-23  
 ; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 1.30  
 ; SEQ ID NO 2  
 ; LENGTH: 839  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-533-220A-2

Query Match 40.3%; Score 1555.5; DB 4; Length 839;  
 Best Local Similarity 44.5%; Pred. No. 5.8e-139;  
 Matches 321; Conservative 137; Mismatches 189; Indels 74; Gaps 12;

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QY 49 PSPADASRPAGGNGRNT-----RMKFG-----APRKGVNPIDLES--TLYSSV 95
DB 22 PDLUDGPNRPPAPKQULSTAKSRTLFGGSGSEEPVYDCPHEBELDSCPTIYVSPV 81
QY 96 V-----PGPKKAPMDSLPDYGYTRHSSDNKRWKRIIEKOPSPAPAPQPPILKVF 149
DB 82 ITTORPDGPTGARL-----LSQSVAASTKRTLR 113
QY 150 NRPLPIVSRGSTADIDGLLPILLTHKKRLTDEEPREPTGKTCPLKALINLSNGNDT 209
DB 114 DRSIFBAVAONNODLESLLFLQSKKHLTNEFPDPTGKTCCLKAMLNLDGQNTT 173
QY 210 IPLLDAERTGNMREPIINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 269
DB 174 IPLLDAERTGNMREPIINSPPFDIYYRGQTALHIAIERCKHYVELLVAGADVHAQAR 233
QY 270 GREFQPDGEGYFPGELPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 329
DB 234 GDEFFKTKGRPGFYFGLPLSLAAGTQPHIVNYLTENPHKADMRQDSRGNTVHALV 293
QY 330 AIDNRENTKFTYKMYDLILKCARLPDSNLEAVLNNDGLSPIMAAATGKIGFOHT 389
DB 294 EVADNTADNTKFTYKMYDLILKCARLPDSNLEAVLNNDGLSPIMAAATGKIGFOHT 353
QY 390 IREEVDEDTRLSRKFKDMAYGVPYSSLYDLSLDTGCEASVLEILVY-NSKIENRHE 448
DB 354 LOREIOBECRHLSRKFKTEWAVGPHVSSLYDLSLDTGCEASVLEILVY-NSKIENRHE 412
QY 449 MAVEPINELLRDKMRKFGAVSFYINVSYLCAWITFTLTAAYQPLEGTPPYRYRTVDY 508
DB 413 MLVEPINELLRDKMRKFGAVSFYINVSYLCAWITFTLTAAYQPLEGTPPYRYRTVDY 472
QY 509 LRLAGEVITLFTGVLFPEFTNICKLFEMKCCPGVNSLFDISGFOLLYFYSVLVISAALYL 568
DB 473 FRTYGLISLVGVSVEFFRGIQ-YFLQRRBSMKTLEFVDSSEMLFLOSLFMLATVLYLF 531
QY 569 AGIEAVLAVWVFLVGMNNAIYTRGLKLTGYTSIMIQIKLFKDFRPLVLYLLPMIGY 628
DB 532 SHKEVYASVWVFLVGMNNAIYTRGLKLTGYTSIMIQIKLFKDFRPLVLYLLPMIGY 591
QY 629 ASALVSLNPCAMKVCNEDQNTCTVPTY-----PSCRDSCT-----FSTFLDLFX 675
DB 592 STAVVTLI-----EDGKNDSLPSSESTSHRWGAPACRPDSSVNSLYST-CLELFX 640
QY 676 LITGMGDLMLSTKYPVFIILVYIILTFVLLNMLIALMGFTVGVGSKESKRIWKL 735
DB 641 FTIGMDLEFTENYDKAVFIILVYIILTFVLLNMLIALMGFTVGVGSKESKRIWKL 700
QY 736 Q 736
DB 701 Q 701

```

RESULT 15  
 US-09-197-636-4  
 ; Sequence 4, Application US/09197636  
 ; Patent No. 6239267  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DUCKWORTH, DAVID  
 ; APPLICANT: HAYES, PHILIP  
 ; APPLICANT: MEADOWS, HELEN  
 ; APPLICANT: DAVIS, JOHN  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Ratner & Prestia  
 ; STREET: P.O. Box 980  
 ; CITY: Valley Forge  
 ; STATE: PA  
 ; COUNTRY: US  
 ; ZIP: 19482-0980  
 ; COMPUTER READABLE FORM:

```

1      MEDIUM TYPE: Diskette
2      COMPUTER: IBM Compatible
3      OPERATING SYSTEM: DOS
4      SOFTWARE: FASTSEQ for Windows Version 2.0.C
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/09/197,636
7      FILING DATE: 23-NOV-1998
8      CLASSIFICATION:
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: UK 9805137.8
11     FILING DATE: 12-MAR-1998
12     APPLICATION NUMBER: UK 9815791.0
13     FILING DATE: 21-JUL-1998
14     APPLICATION NUMBER: UK 9819278.4
15     FILING DATE: 03-SEP-1998
16     ATTORNEY/AGENT INFORMATION:
17     NAME: Prestia, Paul F
18     REGISTRATION NUMBER: 23,031
19     REFERENCE/DOCKET NUMBER: GP-30075
20     TELECOMMUNICATION INFORMATION:
21     TELEPHONE: 601-407-0700
22     TELEFAX: 610-407-0701
23     TELEX: 9461C9
24     INFORMATION FOR SEQ ID NO: 4:
25     SEQUENCE CHARACTERISTICS:
26     LENGTH: 839 amino acids
27     TYPE: amino acid
28     STRANDEDNESS: single
29     TOPOLOGY: linear
30     MOLECULE TYPE: protein
31     US-09-197-636-4

```

Query Match	40.2%;	Score 1552.5;	DB 3;	Length 839;
Best Local Similarity	44.4%;	Pred. No. 1.1e-138;		
Matches 320;	Conservative 189;	Mismatches 189;	Indels 74;	Gaps 12

```

0Y      49 FSPADASRPAGBGRKPNL-----RMKQG-----ARKGVPNIDLES--TLYESSV   95
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      22 PDLPLGDNDNSRPPAKPOLSTAKSRTLRFGKDSEAEFPVDCPHBBEGELSDCPTLYFV    81
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      96 V-----DPPKAPMDSLFDYGTVMHHSNDNRMKKITEKOPSGPKAPAPOPILKYF   149
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      82 ITTORPGDCEFTCARL-----LQDSVAASTEXTRLRY   113
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      150 NEPIIFDIYSRGSTADLDGLIRPELLTHKKRLTDEEFREBSTGTCIPKALINLSGRNDT   209
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      114 DRSRTFEANAQNOCDDLESLILFLQSKSKGHYNEDNEKDBETGCTCLKAMLIHQDMNTT   173
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      210 IPVLIDIAERTGNMBEFINSPFRDIYYRGOTAHIAIERCKHYELLVAQADVAQAOR     269
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      174 IPLLIEIAQOTLSKELVNAXYTDXKKYQOTAHIAIERNNALVTLLVENAQDVQAANH   233
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      270 GRFPQKDGCVFYGEELPFLSLAACINOIHIVNYLTENPHKADMRQDSRGTVLHALV   329
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      234 GPFPEKTGRPGFYGEELPFLSLAACNTOIGIKFELIQNSWQRNDAIBOSVGVTVLHALV   293
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      330 AIADNTRNTKFTKYVDLLILKCARLPEDSNILEAVLNNDGLSPIMMAAKTGKIGIFOHI   389
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      294 EVADNMTADMTKFTVSMYNEIILLIGAKLHPTELKEELTNKKGMTPLALAAGTGITGLAYI   353
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      390 IRREVTDETRHLSRKFQOMAYGPVYSSLYDLSLDTQCBEMSVLEILVY-NKIENRBH   448
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      354 LQREIOEPICRHISRKFTEMAYGPVHSSLYDLSIDTC-EKNSVLVIIVASSETNRHD   412
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      449 MAAVEPIINELHRKMKKFGAVSYFIWNVSYLCAVIFTFLTAAYOPELGTPPYRYRTLVYD   508
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      413 MLAVEPIANLLODKMDRFYKRIIFYFNFVLYCLMYIIFTMAAYIARYPDGLPRFMKXTGYD   472
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      509 LRAGEVITLFTGSVFEEFTNIKDLFMKKCGVNSLFDIGSFOLLTYTFYSVLVISAALI   568
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      473 FYVTGSIILVGSVYFFFRGIC-YFLQBRBSMTKLTFVDSYSEMWLFLOSIFMLATVLYF   531
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      569 AGIEAVLAVMFALVIGMMNALYFTGKLITGYTYSIMICKLEFKDLERFLVYLLFMICY   628

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[illegible]

Search completed: December 2, 2004, 22:36:13  
Job time : 45 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 22:26:51 ; Search time 148 Seconds  
(without alignments)  
1787.935 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858  
Sequence: 1 MADSSGPRAGPGEVAFLE.....GVSKSKHIMWLQSGRRRL 742

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/FCI\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
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  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	14	US-10-090-215-12
2	3829	99.2	831	15	US-10-342-844-76
3	3829	99.2	870	16	US-10-761-065-2
4	3829	99.2	871	10	US-09-870-090-2
5	3829	99.2	871	14	US-10-000-823-7
6	3829	99.2	871	14	US-10-171-319-7
7	3829	99.2	871	15	US-10-342-844-54
8	3829	99.2	871	15	US-10-342-844-58
9	3829	99.2	871	15	US-10-342-844-78
10	3829	99.2	871	17	US-10-415-570A-2
11	3828	99.2	871	14	US-10-027-828-2
12	3828	99.2	871	15	US-10-342-844-60
13	3825	99.1	871	14	US-10-027-828-4

14	3823	99.1	871	14	US-10-090-215-7	Sequence 7, Appli
15	3810	98.8	963	10	US-09-932-165-1477	Sequence 1477, Ap
16	3809	98.7	871	14	US-10-227-255A-3	Sequence 3, Appli
17	3695	95.8	871	15	US-10-342-844-84	Sequence 84, Appli
18	3693	95.7	830	14	US-10-027-828-6	Sequence 6, Appli
19	3693	95.7	871	14	US-10-027-828-11	Sequence 11, Appli
20	3693	95.7	871	15	US-10-342-844-66	Sequence 66, Appli
21	3689	95.6	871	15	US-10-342-844-80	Sequence 80, Appli
22	3687	95.6	871	14	US-10-027-828-10	Sequence 10, Appli
23	3686	95.5	871	14	US-10-027-828-8	Sequence 8, Appli
24	3686	95.5	871	14	US-10-027-828-9	Sequence 9, Appli
25	3685	95.5	871	14	US-10-171-319-14	Sequence 14, Appli
26	3681	95.4	871	14	US-10-227-255A-1	Sequence 1, Appli
27	3652	94.7	870	14	US-10-027-828-13	Sequence 13, Appli
28	3636	94.2	873	15	US-10-342-844-64	Sequence 64, Appli
29	3472	90.0	803	15	US-10-342-844-56	Sequence 56, Appli
30	3470	89.9	811	14	US-10-090-215-9	Sequence 9, Appli
31	3467	89.9	792	9	US-09-764-367A-2	Sequence 2, Appli
32	3457	89.6	803	9	US-09-764-367A-8	Sequence 8, Appli
33	3389	87.8	803	15	US-10-342-844-62	Sequence 62, Appli
34	3284	85.1	852	14	US-10-027-828-15	Sequence 15, Appli
35	3284	85.1	852	15	US-10-342-844-36	Sequence 36, Appli
36	3120	80.9	743	9	US-09-764-367A-11	Sequence 11, Appli
37	3044.5	78.9	734	9	US-09-764-367A-4	Sequence 4, Appli
38	2847	73.8	625	10	US-09-932-165-1507	Sequence 1507, Ap
39	2782	72.1	625	10	US-09-932-165-1506	Sequence 1506, Ap
40	2373.5	61.5	602	10	US-09-870-090-4	Sequence 4, Appli
41	2373.5	61.5	602	16	US-10-761-065-4	Sequence 4, Appli
42	2156.5	55.9	559	14	US-10-297-022-10	Sequence 10, Appli
43	1808	46.9	498	14	US-10-168-651-2	Sequence 2, Appli
44	1622	42.0	420	14	US-10-027-828-7	Sequence 7, Appli
45	1622	42.0	461	14	US-10-027-828-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-10-090-215-12  
Sequence 12, Application US/10090215  
Publication No. US20030032097A1  
GENERAL INFORMATION:  
APPLICANT: Dublin, Adrienne E  
APPLICANT: Huvar, Arne  
APPLICANT: Erlander, Mark G  
APPLICANT: Glaes, Charles A  
TITLE OF INVENTION: VR3  
FILE REFERENCE: Human VR3 receptors  
CURRENT APPLICATION NUMBER: US/10/090,215  
CURRENT FILING DATE: 2002-03-04  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 12  
LENGTH: 742  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-090-215-12

Query Match	100.0%	Score 3858;	DB 14;	Length 742;
Best Local Similarity	100.0%	Pred. No. 1.7e-307;		
Matches 742;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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DB	1	MADSSGPRAGPGEVAFLEPDSGTPGGEAPPLSLANIFEGEDGSLSPSPADASRPAGP	60	
QY	61	GDGPNLTKMKQGAFFKGVNPIDLESTLVSSVVPKPKAPMDSLDYGYRHSSDN	120	
DB	61	GDGPNLTKMKQGAFFKGVNPIDLESTLVSSVVPKPKAPMDSLDYGYRHSSDN	120	
QY	121	KRMKLTLEKQDQSPKADAPQPPILTKVFNPIIFDIYSRGSSTADLDGLPFLTHKKRL	180	



D	121	KMRKRLIEKQGSKAPAPQEPPLIKVENPRLFDIYSRSTADLGLLPLILTHKKL	180
Q	181	TDEEFREPGTKTCLPKALMLNSGRNDTPYLLDIARFCNMRREFINSPPRIYRGQ	240
D	181	TDEEFREPGTKTCLPKALMLNSGRNDTPYLLDIARFCNMRREFINSPPRIYRGQ	240
Q	241	ALHIALERSCKHYVELLVAGADVAQARGFPOCKEGGYFGEGLPLSLAACTQPHI	300
D	241	ALHIALERSCKHYVELLVAGADVAQARGFPOCKEGGYFGEGLPLSLAACTQPHI	300
Q	301	VNYLTENPHKKADMRRODSRGNTVLHAIVALADNTRENTKFTVYQYDLLLKCARLPDS	360
D	301	VNYLTENPHKKADMRRODSRGNTVLHAIVALADNTRENTKFTVYQYDLLLKCARLPDS	360
Q	361	NLEAVLNNGLSPIWMAATGKIGIPOHITREPVDEDTBRLSRKFDMAVGPYSSLYD	420
D	361	NLEAVLNNGLSPIWMAATGKIGIPOHITREPVDEDTBRLSRKFDMAVGPYSSLYD	420
Q	421	LSLSDTCGEBASTLEILVYNSKLIENRHEMLAVEPINELLRDKMRKFGAVSPYINVSILC	480
D	421	LSLSDTCGEBASTLEILVYNSKLIENRHEMLAVEPINELLRDKMRKFGAVSPYINVSILC	480
Q	481	AMVIFTLTAYQPLBEGTPPYPRRTTYDYRLAGEVITTLFGVLPFFNTIKOLFMKKCPGV	540
D	481	AMVIFTLTAYQPLBEGTPPYPRRTTYDYRLAGEVITTLFGVLPFFNTIKOLFMKKCPGV	540
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D	541	NSLPIDGSFOLAFRISVLYVSALYIAGIEAVALVWFAVLVGMNMLFFTRGLKLTG	600
Q	601	TYSIMIOKILFQDLFRRLLVYLLFMIGVASALVSLNPPCANMKVCNEQDNTCTVPTYBSC	660
D	601	TYSIMIOKILFQDLFRRLLVYLLFMIGVASALVSLNPPCANMKVCNEQDNTCTVPTYBSC	660
Q	661	RDSSTFSTFLDLFKLITGMGDEMLSSRKYPVFFILLYYIILTFVLLNMLIALMGE	720
D	661	RDSSTFSTFLDLFKLITGMGDEMLSSRKYPVFFILLYYIILTFVLLNMLIALMGE	720
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D	721	TVGVGSKESKIHIMKLSGRRRL	742

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RESULT 2
US-10-342-844-76
; Sequence 76, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelabi, G'n'l
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 804, 816
; OTHER INFORMATION: Xaa = Any Amino Acid
; PUBLICATION INFORMATION:

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; DATABASE ACCESSION NUMBER: Genbank XP_012261
; DATABASE ENTRY DATE: 2001-10-16
US-10-342-844-76

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Query Match	99.2%	Score 3829;	DB 15;	Length 831;
Best Local Similarity	100.0%	Pred. No. 5e-305;		
Matches 736;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MADSSBGRAPGVAELPGDESGIPQGEAPLSSLANLFEJGDSLSFSPLMASHKAPG	80
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QY	1	MADSSBGRAPGVAELPGDESGIPQGEAPLSSLANLFEJGDSLSFSPLMASHKAPG	120
Db	61	GDGRPNLMMKQGAFFRKGVNPPIDLBESTLYESSVVPCKKAPMDSLDYGYRRHSSDN	120
QY	121	KWRKRIIEKOPQSKAPAPOPPLTKFKNRPILFDIYSRGSSTADLDGLPELTHKKRL	180
Db	121	KWRKRIIEKOPQSKAPAPOPPLTKFKNRPILFDIYSRGSSTADLDGLPELTHKKRL	180
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QY	241	ALHIAIERCKHYVELLYAOGADVAOAKRGPRFQPKDGGYRYPEELPLSLAACNPOPI	300
Db	241	ALHIAIERCKHYVELLYAOGADVAOAKRGPRFQPKDGGYRYPEELPLSLAACNPOPI	300
QY	301	VNYLLENNHHKKADMMRQDSRGNTVHALVALADNRENTKPYTKMYDLLLKCARLFPDS	360
Db	301	VNYLLENNHHKKADMMRQDSRGNTVHALVALADNRENTKPYTKMYDLLLKCARLFPDS	360
QY	361	NLEAVLANNDGSLPLMMAAKTGKIGIFOHIIIRREVTDDETRHLSRKFKDMAVAPVYSSLYD	420
Db	361	NLEAVLANNDGSLPLMMAAKTGKIGIFOHIIIRREVTDDETRHLSRKFKDMAVAPVYSSLYD	420
QY	421	ISSLDTCGEASVLELTYNSKIENRHEMLAVEPINELLRDQMKRKAUSFYTNVYSYC	480
Db	421	ISSLDTCGEASVLELTYNSKIENRHEMLAVEPINELLRDQMKRKAUSFYTNVYSYC	480
QY	481	ANVIFLTAAYQPBGSTPPYPRKTYVDYRLAGEVITLFTGYLFFPTNJKDLFMKKCPGV	540
Db	481	ANVIFLTAAYQPBGSTPPYPRKTYVDYRLAGEVITLFTGYLFFPTNJKDLFMKKCPGV	540
QY	541	NSLTFIDGSPQLTYFYTSVLIVISAALYLAGIEBAYLAVMFAVLGMNMLFYTRGLKTG	600
Db	541	NSLTFIDGSPQLTYFYTSVLIVISAALYLAGIEBAYLAVMFAVLGMNMLFYTRGLKTG	600
QY	601	TYSIMIOKLLFKYDLFRFLLVYLLFMGYASALVSLNPPCANMVCNEDQNTCPVYPSC	666
Db	601	TYSIMIOKLLFKYDLFRFLLVYLLFMGYASALVSLNPPCANMVCNEDQNTCPVYPSC	666
QY	661	RQSEFTSTLLDFKLLTGMGDLEMSTRKYPVFFILLVYTYLLFVLLANMLALMGE	720
Db	661	RQSEFTSTLLDFKLLTGMGDLEMSTRKYPVFFILLVYTYLLFVLLANMLALMGE	720
QY	721	TVQGVSKESHKWLKQ 736	
Db	721	TVQGVSKESHKWLKQ 736	

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RESULT 3
US-10-761-065-2
; Sequence 2, Application US/10761065
; Publication No. US20040137573A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; APPLICANT: Katsuhiko Shinjo
; APPLICANT: Hikaru Yabuchi
; TITLE OF INVENTION: Human Vanilloid Receptor-like Proteins
; FILE REFERENCE: PC9799ADAM
; CURRENT APPLICATION NUMBER: US/10/761, 065
; CURRENT FILING DATE: 2004-01-20

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; PRIOR APPLICATION NUMBER: US/09/870,090A  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/208,156  
 ; PRIOR FILING DATE: 2000-05-31  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 870  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-10-761-065-2

Query Match 99.2%; Score 3829; DB 16; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-305;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MADSSGPRAGGEVAVELPGDESGTGGGAFFPLSLANLFEEDGSLSPSPADASRPAGP 60
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DB 61 GGRPPLRMKFGAFAKGVNPIIDLESTLYESSVPGPKAPMDSLFDYGYRHSSDN 120
QY 121 KWRKKLIEKOPSPKAPAPQPPILKVENRPIIFDIVSGSTADLDGLPFLTHKKL 180
DB 121 KWRKKLIEKOPSPKAPAPQPPILKVENRPIIFDIVSGSTADLDGLPFLTHKKL 180
QY 181 TDEEFEPSTGTCIPKALNLSNGRNDTIPVLIDIAERTGNMREINSPFRDIYRGOT 240
DB 181 TDEEFEPSTGTCIPKALNLSNGRNDTIPVLIDIAERTGNMREINSPFRDIYRGOT 240
QY 241 ALHAIERRCKHYVELVAQADVAQAARGFPQKDEGGYFEGELPLSLAQTNPPI 300
DB 241 ALHAIERRCKHYVELVAQADVAQAARGFPQKDEGGYFEGELPLSLAQTNPPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKMDLLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKMDLLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMMAAKTGKIGI FOHIIRREVTDEDRHLSRKFKMAAYGPVYSSLYD 420
DB 361 NLEAVLNNDGSLPLMMAAKTGKIGI FOHIIRREVTDEDRHLSRKFKMAAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
QY 481 AMVITTLTAAYQPLEGTPEPYRTTVDYIRLAGEVITLFTGVLPFFTNIKDLFMKCPGV 540
DB 481 AMVITTLTAAYQPLEGTPEPYRTTVDYIRLAGEVITLFTGVLPFFTNIKDLFMKCPGV 540
QY 541 NSLFDGSGFOLLFYTSVLYVISAALYLAGIEAYAVAVWVFAVLGMMNALVYTRGKLTG 600
DB 541 NSLFDGSGFOLLFYTSVLYVISAALYLAGIEAYAVAVWVFAVLGMMNALVYTRGKLTG 600
QY 601 TYSIMIQILFKDLFRFLVYLLEFMIGYASALVSLNFCAMNKVCNEQNTCTVPTPSC 660
DB 601 TYSIMIQILFKDLFRFLVYLLEFMIGYASALVSLNFCAMNKVCNEQNTCTVPTPSC 660
QY 661 RDSEFPSTFLDLFDLITGMGDEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
DB 661 RDSEFPSTFLDLFDLITGMGDEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
QY 721 TVGVSKSKSHIMKIQ 736
DB 721 TVGVSKSKSHIMKIQ 736

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RESULT 4  
 US-09-870-090-2  
 ; Sequence 2, Application US/09870090  
 ; Publication No. US20030017527A1

; GENERAL INFORMATION:  
 ; APPLICANT: Pfizer Product Inc.  
 ; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins  
 ; FILE REFERENCE: PC9979A  
 ; CURRENT APPLICATION NUMBER: US/09/870,090  
 ; CURRENT FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/208,156  
 ; PRIOR FILING DATE: 2000-05-31  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 871  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-870-090-2

Query Match 99.2%; Score 3829; DB 10; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-305;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADSSGPRAGGEVAVELPGDESGTGGGAFFPLSLANLFEEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGGEVAVELPGDESGTGGGAFFPLSLANLFEEDGSLSPSPADASRPAGP 60
QY 61 GGRPPLRMKFGAFAKGVNPIIDLESTLYESSVPGPKAPMDSLFDYGYRHSSDN 120
DB 61 GGRPPLRMKFGAFAKGVNPIIDLESTLYESSVPGPKAPMDSLFDYGYRHSSDN 120
QY 121 KWRKKLIEKOPSPKAPAPQPPILKVENRPIIFDIVSGSTADLDGLPFLTHKKL 180
DB 121 KWRKKLIEKOPSPKAPAPQPPILKVENRPIIFDIVSGSTADLDGLPFLTHKKL 180
QY 181 TDEEFEPSTGTCIPKALNLSNGRNDTIPVLIDIAERTGNMREINSPFRDIYRGOT 240
DB 181 TDEEFEPSTGTCIPKALNLSNGRNDTIPVLIDIAERTGNMREINSPFRDIYRGOT 240
QY 241 ALHAIERRCKHYVELVAQADVAQAARGFPQKDEGGYFEGELPLSLAQTNPPI 300
DB 241 ALHAIERRCKHYVELVAQADVAQAARGFPQKDEGGYFEGELPLSLAQTNPPI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKMDLLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRNTKFTYKMDLLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMMAAKTGKIGI FOHIIRREVTDEDRHLSRKFKMAAYGPVYSSLYD 420
DB 361 NLEAVLNNDGSLPLMMAAKTGKIGI FOHIIRREVTDEDRHLSRKFKMAAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDCKRKGAVSFYINVSYLEC 480
QY 481 AMVITTLTAAYQPLEGTPEPYRTTVDYIRLAGEVITLFTGVLPFFTNIKDLFMKCPGV 540
DB 481 AMVITTLTAAYQPLEGTPEPYRTTVDYIRLAGEVITLFTGVLPFFTNIKDLFMKCPGV 540
QY 541 NSLFDGSGFOLLFYTSVLYVISAALYLAGIEAYAVAVWVFAVLGMMNALVYTRGKLTG 600
DB 541 NSLFDGSGFOLLFYTSVLYVISAALYLAGIEAYAVAVWVFAVLGMMNALVYTRGKLTG 600
QY 601 TYSIMIQILFKDLFRFLVYLLEFMIGYASALVSLNFCAMNKVCNEQNTCTVPTPSC 660
DB 601 TYSIMIQILFKDLFRFLVYLLEFMIGYASALVSLNFCAMNKVCNEQNTCTVPTPSC 660
QY 661 RDSEFPSTFLDLFDLITGMGDEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
DB 661 RDSEFPSTFLDLFDLITGMGDEMLSTKYPVVFIIILVYIIITFVLLNMLTALMGE 720
QY 721 TVGVSKSKSHIMKIQ 736
DB 721 TVGVSKSKSHIMKIQ 736

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QY 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPINELLDRKMRKGAVSFYINVSYLQ 480
DB 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPINELLDRKMRKGAVSFYINVSYLQ 480
QY 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKCCPGV 540
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QY 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
QY 601 TYSIMOKLIFKDLFFLLVYLLFMIGYASALVSLINPCANMKVCNEDQTNCTVPTYPSC 660
DB 601 TYSIMOKLIFKDLFFLLVYLLFMIGYASALVSLINPCANMKVCNEDQTNCTVPTYPSC 660
QY 661 RSESTFSTLDDLFLKTIGMDLEMLSTKYVVFVFIILVYIILFVLLINMLIALMGE 720
DB 661 RSESTFSTLDDLFLKTIGMDLEMLSTKYVVFVFIILVYIILFVLLINMLIALMGE 720
QY 721 TVGOVSKESKHIMKLO 736
DB 721 TVGOVSKESKHIMKLO 736

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## RESULT 7

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US-10-342-844-54
; Sequence 54, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Staudeman, Kenneth
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 871
; TYPE: PRF
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Genbank XP_027181
; DATABASE ENTRY DATE: 2002-09-01
US-10-342-844-54

```

```

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MADSEGPAGGAEVLAELPGDESGTPGGAFLSLANLFEEDDSLSRSPADASRPAP 60
DB 1 MADSEGPAGGAEVLAELPGDESGTPGGAFLSLANLFEEDDSLSRSPADASRPAP 60
QY 61 GGGRENLMKFGAARKGVPNPIDLESTLYESSVVPCKAPMDSLFDYGYRRHSSDN 120
DB 61 GGGRENLMKFGAARKGVPNPIDLESTLYESSVVPCKAPMDSLFDYGYRRHSSDN 120
QY 121 KMRKXIIIEKOPSPKAPAPPPILKVNRPILFDIYRSGSTADLDGLLPFLTHKKKL 180
DB 121 KMRKXIIIEKOPSPKAPAPPPILKVNRPILFDIYRSGSTADLDGLLPFLTHKKKL 180
QY 181 TDEEFPSTGTCLPKALNLSNGRNDIIPVLLDIABRTGMRRRINSPPFDIYYRGQT 240
DB 181 TDEEFPSTGTCLPKALNLSNGRNDIIPVLLDIABRTGMRRRINSPPFDIYYRGQT 240

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DB 181 TDEEFPSTGTCLPKALNLSNGRNDIIPVLLDIABRTGMRRRINSPPFDIYYRGQT 240
QY 241 ALHIAIERCKKHVELLVQAGADVHAQGRFPQPDGQYFPGSLPLSLACTOPHI 300
DB 241 ALHIAIERCKKHVELLVQAGADVHAQGRFPQPDGQYFPGSLPLSLACTOPHI 300
QY 301 VNVLTENPKKADMRQDSRGNTVLAVALADNTRNTKFKYKMTDLILKCARLPDS 360
DB 301 VNVLTENPKKADMRQDSRGNTVLAVALADNTRNTKFKYKMTDLILKCARLPDS 360
QY 361 NIEAVLNNDGLSPIMAAATGKIGIFQHIIRREVTEDTRHLSRKKEDMAAYGVSSLYD 420
DB 361 NIEAVLNNDGLSPIMAAATGKIGIFQHIIRREVTEDTRHLSRKKEDMAAYGVSSLYD 420
QY 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPINELLDRKMRKGAVSFYINVSYLQ 480
DB 421 LSLDTCGEASVLEILVNSKIENRHEMLAVEPINELLDRKMRKGAVSFYINVSYLQ 480
QY 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKCCPGV 540
DB 481 AMVIFTLTAAYOPLBEGTPPYRTTYDYLRLAGEVITLFTGVLFETTNIKDLFMKCCPGV 540
QY 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAWVPALVGMNMLYFTRGLKLTG 600
QY 601 TYSIMOKLIFKDLFFLLVYLLFMIGYASALVSLINPCANMKVCNEDQTNCTVPTYPSC 660
DB 601 TYSIMOKLIFKDLFFLLVYLLFMIGYASALVSLINPCANMKVCNEDQTNCTVPTYPSC 660
QY 661 RSESTFSTLDDLFLKTIGMDLEMLSTKYVVFVFIILVYIILFVLLINMLIALMGE 720
DB 661 RSESTFSTLDDLFLKTIGMDLEMLSTKYVVFVFIILVYIILFVLLINMLIALMGE 720
QY 721 TVGOVSKESKHIMKLO 736
DB 721 TVGOVSKESKHIMKLO 736

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## RESULT 8

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US-10-342-844-58
; Sequence 58, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Staudeman, Kenneth
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 871
; TYPE: PRF
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Genbank BAB69040
; DATABASE ENTRY DATE: 2001-10-02
US-10-342-844-58

```

```

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	1	MADSESEGRAGGEVAELPGDESGTGGGAFLSSIANFEEGEDGSLSSPADASRPAP	60
Db	1	MADSESEGRAGGEVAELPGDESGTGGGAFLSSIANFEEGEDGSLSSPADASRPAP	60
QY	61	GDGRPNLPMKTOGAFRKGVPNPIDLESTLYSSVPGPKAPMDSLPDYGYRRHSSDN	120
Db	61	GDGRPNLPMKTOGAFRKGVPNPIDLESTLYSSVPGPKAPMDSLPDYGYRRHSSDN	120
QY	121	KMRKKIIEKOPQSPKAPAPOPPILIKVNNRPLFDIVRGSTADIDGLLPLTLTKKRL	180
Db	121	KMRKKIIEKOPQSPKAPAPOPPILIKVNNRPLFDIVRGSTADIDGLLPLTLTKKRL	180
QY	181	TDEEFREBPTGKTCLPKALLNSNGNDTIPLYLDIAERTGNMREFINSPFRDIYRGQT	240
Db	181	TDEEFREBPTGKTCLPKALLNSNGNDTIPLYLDIAERTGNMREFINSPFRDIYRGQT	240
QY	241	ALHIAIERCKHYVELLVQAQADYHAQAARGFPOPBDEGYEFYFGLPLSLAATNOPHI	300
Db	241	ALHIAIERCKHYVELLVQAQADYHAQAARGFPOPBDEGYEFYFGLPLSLAATNOPHI	300
QY	301	VNYLTENPHKKADMRQDSRGNTVLAVALADNTEENTKFTVMYDILLKCARLPDS	360
Db	301	VNYLTENPHKKADMRQDSRGNTVLAVALADNTEENTKFTVMYDILLKCARLPDS	360
QY	361	NLEAVLNDGSLPLMMAATGKIGIFQHIIRREYDEBTRHLSRKKQMAVGYVSSLYD	420
Db	361	NLEAVLNDGSLPLMMAATGKIGIFQHIIRREYDEBTRHLSRKKQMAVGYVSSLYD	420
QY	421	LSLSLTGCEASVLELTVNSKTIENHEMLAVERINELRDKRKKGAVSYINVSYL	480
Db	421	LSLSLTGCEASVLELTVNSKTIENHEMLAVERINELRDKRKKGAVSYINVSYL	480
QY	481	AMVIFTLTAAYOPLEGTPPYKRTIVDYRLAGEVITLFTGVLPFTNIXDLMFKKCPGV	540
Db	481	AMVIFTLTAAYOPLEGTPPYKRTIVDYRLAGEVITLFTGVLPFTNIXDLMFKKCPGV	540
QY	541	NSLFIIDSGQOLLYFYISVAVTSAALYLAGIBAYLAWMPALVGMNNALYFRGLKLTG	600
Db	541	NSLFIIDSGQOLLYFYISVAVTSAALYLAGIBAYLAWMPALVGMNNALYFRGLKLTG	600
QY	601	TYSIMIOKILFKDPRFRLIVYLLFMIGYASALVSLNPMCANMKVCNEDQNTCTVPTPSC	660
Db	601	TYSIMIOKILFKDPRFRLIVYLLFMIGYASALVSLNPMCANMKVCNEDQNTCTVPTPSC	660
QY	661	RDSERFSTLIDLFLKLTIGMDLEMLSTKYPVFIILVTYIILTFVLLNMLALMGE	720
Db	661	RDSERFSTLIDLFLKLTIGMDLEMLSTKYPVFIILVTYIILTFVLLNMLALMGE	720
QY	721	TVGOVSKESHIMKLG 736	
Db	721	TVGOVSKESHIMKLG 736	
RESULT 9			
US-10-342-844-78			
; Sequence 78, Application US/10342844			
; Publication No. US20040009537A1			
GENERAL INFORMATION:			
; APPLICANT: Koos, Jack			
; APPLICANT: Staudeman, Kenneth			
; APPLICANT: Velicelebi, G'n 1			
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING			
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM			
; FILE REFERENCE: 37481-3307			
; CURRENT APPLICATION NUMBER: US/10/342, 844			
; CURRENT FILING DATE: 2003-01-13			
; PRIOR APPLICATION NUMBER: US 60/347,459			
; PRIOR FILING DATE: 2002-01-11			
; PRIOR APPLICATION NUMBER: US 60/401,171			
; PRIOR FILING DATE: 2002-08-02			
; PRIOR APPLICATION NUMBER: US 60/405,678			
; PRIOR FILING DATE: 2002-08-20			
; NUMBER OF SEQ ID NOS: 115			

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; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO: 78
; LENGTH: 871
; TYPE: PRF
; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AM616127
; DATABASE ENTRY DATE: 2000-09-26
; US-10-342-844-78

Query Match      99.2%  Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 5.3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 MADSSSEGPRAAGPGEVAELPGDESGTGGGAEPPLSSLANLFECEGDSLSPSPADASRPAGP 60
DB      1 MADSSSEGPRAAGPGEVAELPGDESGTGGGAEPPLSSLANLFECEGDSLSPSPADASRPAGP 60

QY      61 GDGPNLRMRFQGAERKGVNPRIDLESTLYESSVVPKKAPMDSLFDYGYRRHSSDN 120
DB      61 GDGPNLRMRFQGAERKGVNPRIDLESTLYESSVVPKKAPMDSLFDYGYRRHSSDN 120

QY      121 KRWKRLIIERKQPGAPKAPAPQPPILKVENRPIFDIVSRGSTADLDGLPELITHKRL 180
DB      121 KRWKRLIIERKQPGAPKAPAPQPPILKVENRPIFDIVSRGSTADLDGLPELITHKRL 180

QY      181 TDEEFREPSGTGCTCPKALNLSNGRDTITVLLDIARTGNMRFINSPPFDIYYRQT 240
DB      181 TDEEFREPSGTGCTCPKALNLSNGRDTITVLLDIARTGNMRFINSPPFDIYYRQT 240

QY      241 ALHAIARRCHYVELVAQGAADVAQAQRFPQPKDGGFYFBEPLPLSLAAGTNOPIH 300
DB      241 ALHAIARRCHYVELVAQGAADVAQAQRFPQPKDGGFYFBEPLPLSLAAGTNOPIH 300

QY      301 VNYLTENPHKKADNRQDSRGNTVLAALVADNTRENTKFTKMYDILLKCARLFPDS 360
DB      301 VNYLTENPHKKADNRQDSRGNTVLAALVADNTRENTKFTKMYDILLKCARLFPDS 360

QY      361 NLEAVLNNDGSLPLMAAKTGKIGI FGHIIIRPVTDENTRHLSRKFQMAVGPVYSSLYD 420
DB      361 NLEAVLNNDGSLPLMAAKTGKIGI FGHIIIRREVTDENTRHLSRKFQMAVGPVYSSLYD 420

QY      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSYINVSYYC 480
DB      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSYINVSYYC 480

QY      481 AMVIFLTATYQPILEGTPPYRRTVDRLAGEVITLTFTGLFFFTNKKDLPMKKCPGV 540
DB      481 AMVIFLTATYQPILEGTPPYRRTVDRLAGEVITLTFTGLFFFTNKKDLPMKKCPGV 540

QY      541 NSLFDIGSFQLLFYFVSVLVSALVYAGIEAYLAWVFAVLVLGMNALYFTRGKLNG 600
DB      541 NSLFDIGSFQLLFYFVSVLVSALVYAGIEAYLAWVFAVLVLGMNALYFTRGKLNG 600

QY      601 TYSINTQKILPFKDLFRFLVYLLEMTGYASALVSLNRCANMKVCNEQDTCVPRYPBC 660
DB      601 TYSINTQKILPFKDLFRFLVYLLEMTGYASALVSLNRCANMKVCNEQDTCVPRYPBC 660

QY      661 RDSEFFSFELLDFPLDTIGMGDLIEMLSSTKYVVFIIILVYIIILTFVLLNMLIALMGE 720
DB      661 RDSEFFSFELLDFPLDTIGMGDLIEMLSSTKYVVFIIILVYIIILTFVLLNMLIALMGE 720

QY      721 TVGQVSKESKHIWKIQ 736
DB      721 TVGQVSKESKHIWKIQ 736

RESULT 10
US-10-415-570A-2
; Sequence 2, Application US/10415570A
; Publication No. US20040198649A1
; GENERAL INFORMATION:
; APPLICANT: Davis, John Beresford

```

; APPLICANT: Gunthorpe, Martin James  
 ; APPLICANT: Egerton, Julie  
 ; APPLICANT: Smart, Darren  
 ; TITLE OF INVENTION: New Use  
 ; FILE REFERENCE: P32689  
 ; CURRENT APPLICATION NUMBER: US/10/415,570A  
 ; CURRENT FILING DATE: 2003-04-23  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/04739  
 ; PRIOR FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: GB 0026114.9  
 ; PRIOR FILING DATE: 2000-10-25  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-415-570A-2

Query Match 99.2%; Score 3829; DB 17; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-305;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGPGEVAVELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60  
 DB 1 MADSSGPRAGPGEVAVELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60  
 QY 61 GGRPPLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAPMDSLFDYGYRHHSSDN 120  
 DB 61 GGRPPLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAPMDSLFDYGYRHHSSDN 120  
 QY 121 KWRKKTIIEKQSPAPAPQPPILKVRNPILFDIVSRGSTADLDGLPLLTTHKKRL 180  
 DB 121 KWRKKTIIEKQSPAPAPQPPILKVRNPILFDIVSRGSTADLDGLPLLTTHKKRL 180  
 QY 181 TDEEFEPSTGKTCLEKALINLSNGRNDITPVLDIAERTGNRRETFINSFPRDIYYRGOT 240  
 DB 181 TDEEFEPSTGKTCLEKALINLSNGRNDITPVLDIAERTGNRRETFINSFPRDIYYRGOT 240  
 QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYFGEPLSLAACTNQPHI 300  
 DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYFGEPLSLAACTNQPHI 300  
 QY 301 VNYLTENPKKADMRQDSRGNTVLAHALVAIADNTEENTKFTYKMYDLILLKCARLFPDS 360  
 DB 301 VNYLTENPKKADMRQDSRGNTVLAHALVAIADNTEENTKFTYKMYDLILLKCARLFPDS 360  
 QY 361 NIEAVLNNDGLSPLMMAATGKIGIFQHIIRREVTDIEDTRHLSRKKRDMAYGCVSYSLVD 420  
 DB 361 NIEAVLNNDGLSPLMMAATGKIGIFQHIIRREVTDIEDTRHLSRKKRDMAYGCVSYSLVD 420  
 QY 421 LSSLDTCGGEASVLEILVYNSKIENHHEMLAVEPINELLRDKWRKFGAVSFYINVSYYC 480  
 DB 421 LSSLDTCGGEASVLEILVYNSKIENHHEMLAVEPINELLRDKWRKFGAVSFYINVSYYC 480  
 QY 481 AVNIFLTAAVYQPLEGTPPYPRRTVDYRLAGEVITLFTGVLPFTTNIKDLFMKKCPGV 540  
 DB 481 AVNIFLTAAVYQPLEGTPPYPRRTVDYRLAGEVITLFTGVLPFTTNIKDLFMKKCPGV 540  
 QY 541 NSLFLDGSFQLLYFYISVAVISAALYLAGIEAYLAVMFALVIGMNNALYFTRGKLKG 600  
 DB 541 NSLFLDGSFQLLYFYISVAVISAALYLAGIEAYLAVMFALVIGMNNALYFTRGKLKG 600  
 QY 601 TYSIMIOKILFKDLRFLLVYLLFMIGYASALVSLNPCANMKVCNEODNCTVPTYPSC 660  
 DB 601 TYSIMIOKILFKDLRFLLVYLLFMIGYASALVSLNPCANMKVCNEODNCTVPTYPSC 660  
 QY 661 ROSEFTSTFLDLFLKLTIGKGDLEMLSTKYPVVFIILLVYIILLFVLLINMLIALMGE 720  
 DB 661 ROSEFTSTFLDLFLKLTIGKGDLEMLSTKYPVVFIILLVYIILLFVLLINMLIALMGE 720  
 QY 721 TVGVSKESKHTWKLO 736  
 DB 721 TVGVSKESKHTWKLO 736

DB 721 TVGVSKESKHTWKLO 736

RESULT 11  
 US-10-027-828-2  
 ; Sequence 2, Application US/10027828  
 ; Publication No. US20030013650A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liedtke, Wolfgang  
 ; APPLICANT: Heller, Stefan  
 ; APPLICANT: Hudspeth, Albert J.  
 ; APPLICANT: Friedman, Jeffrey M.  
 ; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL, PROTEIN, NUCLEIC ACIDS  
 ; FILE REFERENCE: 600-1-287N  
 ; CURRENT APPLICATION NUMBER: US/10/027,828  
 ; CURRENT FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/243,568  
 ; PRIOR FILING DATE: 2000-10-26  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-027-828-2

Query Match 99.2%; Score 3828; DB 14; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 6.4e-305;  
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGPGEVAVELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60  
 DB 1 MADSSGPRAGPGEVAVELPDDESGTGGGAFFPLSSLANLFEGBDGLSPSPADASRPAGP 60  
 QY 61 GGRPPLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAPMDSLFDYGYRHHSSDN 120  
 DB 61 GGRPPLRMKFOGAFKGVNPIIDLESTLYESSVVPGRKAPMDSLFDYGYRHHSSDN 120  
 QY 121 KWRKKTIIEKQSPAPAPQPPILKVRNPILFDIVSRGSTADLDGLPLLTTHKKRL 180  
 DB 121 KWRKKTIIEKQSPAPAPQPPILKVRNPILFDIVSRGSTADLDGLPLLTTHKKRL 180  
 QY 181 TDEEFEPSTGKTCLEKALINLSNGRNDITPVLDIAERTGNRRETFINSFPRDIYYRGOT 240  
 DB 181 TDEEFEPSTGKTCLEKALINLSNGRNDITPVLDIAERTGNRRETFINSFPRDIYYRGOT 240  
 QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYFGEPLSLAACTNQPHI 300  
 DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPDGEGYFYFGEPLSLAACTNQPHI 300  
 QY 301 VNYLTENPKKADMRQDSRGNTVLAHALVAIADNTEENTKFTYKMYDLILLKCARLFPDS 360  
 DB 301 VNYLTENPKKADMRQDSRGNTVLAHALVAIADNTEENTKFTYKMYDLILLKCARLFPDS 360  
 QY 361 NIEAVLNNDGLSPLMMAATGKIGIFQHIIRREVTDIEDTRHLSRKKRDMAYGCVSYSLVD 420  
 DB 361 NIEAVLNNDGLSPLMMAATGKIGIFQHIIRREVTDIEDTRHLSRKKRDMAYGCVSYSLVD 420  
 QY 421 LSSLDTCGGEASVLEILVYNSKIENHHEMLAVEPINELLRDKWRKFGAVSFYINVSYYC 480  
 DB 421 LSSLDTCGGEASVLEILVYNSKIENHHEMLAVEPINELLRDKWRKFGAVSFYINVSYYC 480  
 QY 481 AVNIFLTAAVYQPLEGTPPYPRRTVDYRLAGEVITLFTGVLPFTTNIKDLFMKKCPGV 540  
 DB 481 AVNIFLTAAVYQPLEGTPPYPRRTVDYRLAGEVITLFTGVLPFTTNIKDLFMKKCPGV 540  
 QY 541 NSLFLDGSFQLLYFYISVAVISAALYLAGIEAYLAVMFALVIGMNNALYFTRGKLKG 600  
 DB 541 NSLFLDGSFQLLYFYISVAVISAALYLAGIEAYLAVMFALVIGMNNALYFTRGKLKG 600  
 QY 601 TYSIMIOKILFKDLRFLLVYLLFMIGYASALVSLNPCANMKVCNEODNCTVPTYPSC 660  
 DB 601 TYSIMIOKILFKDLRFLLVYLLFMIGYASALVSLNPCANMKVCNEODNCTVPTYPSC 660



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Db 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNCVPTYPSC 660
Qy 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNLMLALMGE 720
Db 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNLMLALMGE 720
Qy 721 TVGQVSKESKHIWKLQ 736
Db 721 TVGQVSKESKHIWKLQ 736

RESULT 12
US-10-342-844-60
; Sequence 60, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Stauderman, Jack
; APPLICANT: Velleceleb1, G'n_1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG28029
; DATABASE ENTRY DATE: 2000-10-31
US-10-342-844-60

Query Match 99.2%; Score 3828; DB 15; Length 871;
Best Local Similarity 99.9%; Pred. No. 6.4e-305;
Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSBGPRAQPGVAELPGDESGTSGEAFPLSLANLFBGEGDGLSPSPADASRPAGP 60
Db 1 MADSSBGPRAQPGVAELPGDESGTSGEAFPLSLANLFBGEGDGLSPSPADASRPAGP 60
Qy 61 GDGRPNLRMKFOGAFRKGVPNPIDLESTLYESSVVGPKKAPMDSLFDYGTYYRHSSDN 120
Db 61 GDGRPNLRMKFOGAFRKGVPNPIDLESTLYESSVVGPKKAPMDSLFDYGTYYRHSSDN 120
Qy 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Db 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Qy 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Db 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Qy 181 TDEEFREPSTGKTCPLRALNLNSGRNDTIPVLLDIAERTGNMREFFINSPPRDIYYGQT 240
Db 181 TDEEFREPSTGKTCPLRALNLNSGRNDTIPVLLDIAERTGNMREFFINSPPRDIYYGQT 240
Qy 241 ALHTAIRRCRKHVYELLVAQADYHAQARGFFQPKDEGGYFYFGEIPLSLAAGTNOPI 300
Db 241 ALHTAIRRCRKHVYELLVAQADYHAQARGFFQPKDEGGYFYFGEIPLSLAAGTNOPI 300
Qy 301 VNYITANPHKADMRDSDRGNTVLAHALVAADTRETETKVTGMVYDILLKCARLPDS 360
Db 301 VNYITANPHKADMRDSDRGNTVLAHALVAADTRETETKVTGMVYDILLKCARLPDS 360
Qy 301 VNYITANPHKADMRDSDRGNTVLAHALVAADTRETETKVTGMVYDILLKCARLPDS 360
Db 301 VNYITANPHKADMRDSDRGNTVLAHALVAADTRETETKVTGMVYDILLKCARLPDS 360
Qy 361 NLEAVLNNDGLSPIMMAAKTGIGIHOHIIREVLTDEDETRHLSRKKFKDMAYGPIYSSLYD 420
Db 361 NLEAVLNNDGLSPIMMAAKTGIGIHOHIIREVLTDEDETRHLSRKKFKDMAYGPIYSSLYD 420
```

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Qy 421 LSLDTCGEBAVLEILVYNSKIENHEMLAVPINELJDKXKRGAVSFYINVSYL 480
Db 421 LSLDTCGEBAVLEILVYNSKIENHEMLAVPINELJDKXKRGAVSFYINVSYL 480
Qy 481 AMVIFILITAYOOLBEGTPPYRTTYDYRLAEGVTLTFNGULFFFTNIIDLPMKCPGV 540
Db 481 AMVIFILITAYOOLBEGTPPYRTTYDYRLAEGVTLTFNGULFFFTNIIDLPMKCPGV 540
Qy 541 NSLFDGSPOLLYFYISVLYVSAALYAGIEAYLAWMVPAVLGMNNALYFRGLKLTG 600
Db 541 NSLFDGSPOLLYFYISVLYVSAALYAGIEAYLAWMVPAVLGMNNALYFRGLKLTG 600
Qy 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNCVPTYPSC 660
Db 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQNCVPTYPSC 660
Qy 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNLMLALMGE 720
Db 661 RDESETSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNLMLALMGE 720
Qy 721 TVGQVSKESKHIWKLQ 736
Db 721 TVGQVSKESKHIWKLQ 736

RESULT 13
US-10-027-828-4
; Sequence 4, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspecht, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: IT AND USES THEREOF
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-4

Query Match 99.1%; Score 3825; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 1.1e-304;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADSSBGPRAQPGVAELPGDESGTSGEAFPLSLANLFBGEGDGLSPSPADASRPAGP 60
Db 1 MADSSBGPRAQPGVAELPGDESGTSGEAFPLSLANLFBGEGDGLSPSPADASRPAGP 60
Qy 61 GDGRPNLRMKFOGAFRKGVPNPIDLESTLYESSVVGPKKAPMDSLFDYGTYYRHSSDN 120
Db 61 GDGRPNLRMKFOGAFRKGVPNPIDLESTLYESSVVGPKKAPMDSLFDYGTYYRHSSDN 120
Qy 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Db 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Qy 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Db 121 KRWAKKIIIEKQPSKAPAPQPPILKVFNNPILFDIVSRGSTADLGLLPFLTHKKRL 180
Qy 181 TDEEFREPSTGKTCPLRALNLNSGRNDTIPVLLDIAERTGNMREFFINSPPRDIYYGQT 240
Db 181 TDEEFREPSTGKTCPLRALNLNSGRNDTIPVLLDIAERTGNMREFFINSPPRDIYYGQT 240
Qy 181 TDEEFREPSTGKTCPLRALNLNSGRNDTIPVLLDIAERTGNMREFFINSPPRDIYYGQT 240
Db 181 TDEEFREPSTGKTCPLRALNLNSGRNDTIPVLLDIAERTGNMREFFINSPPRDIYYGQT 240
Qy 241 ALHTAIRRCRKHVYELLVAQADYHAQARGFFQPKDEGGYFYFGEIPLSLAAGTNOPI 300
Db 241 ALHTAIRRCRKHVYELLVAQADYHAQARGFFQPKDEGGYFYFGEIPLSLAAGTNOPI 300
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QY 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTENTKFTVKMTDLLLKKCARLPDS 360  
 Db 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTENTKFTVKMTDLLLKKCARLPDS 360  
 QY 361 NLEAVANNNDGSLPMAAAKTGKIGIFOHIIIRREVTEDETRHSRKFKDMAVGVVSSLYD 420  
 Db 361 NLEAVANNNDGSLPMAAAKTGKIGIFOHIIIRREVTEDETRHSRKFKDMAVGVVSSLYD 420  
 QY 421 LSSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSFYINVSYL 480  
 Db 421 LSSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSFYINVSYL 480  
 QY 481 AMVIFTLTAAYOPLGEGTPPYRTTYDYRLAGEVITLFTGVLFPTNKKDLPMKKCPGV 540  
 Db 481 AMVIFTLTAAYOPLGEGTPPYRTTYDYRLAGEVITLFTGVLFPTNKKDLPMKKCPGV 540  
 QY 541 NSLFDGSPQLYFYISVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600  
 Db 541 NSLFDGSPQLYFYISVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600  
 QY 601 TYSIMIOKILFKDLRFELLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660  
 Db 601 TYSIMIOKILFKDLRFELLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660  
 QY 661 RDSFTFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720  
 Db 661 RDSFTFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720  
 QY 721 TVGVSKESKSHIWKLO 736  
 Db 721 TVGVSKESKSHIWKLO 736

## RESULT 14

US-10-090-215-7  
 ; Sequence 7, Application US/10090215  
 ; Publication No. US20030032097A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dublin, Adrienne E  
 ; APPLICANT: Huvart, Arne  
 ; APPLICANT: Erlander, Mark G  
 ; APPLICANT: Glaes, Charles A  
 ; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor  
 ; TITLE OF INVENTION: VR3  
 ; FILE REFERENCE: Human VR3 receptors  
 ; CURRENT APPLICATION NUMBER: US/10/090,215  
 ; CURRENT FILING DATE: 2002-03-04  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-090-215-7

Query Match 99.1%; Score 3823; DB 14; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 1.7e-304;  
 Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MADSEGRAPGGEVAHLPDESCTPGGEAPPLSLANLFGEDGSLSPSPADSRPAGP 60  
 Db 1 MADSEGRAPGGEVAHLPDESCTPGGEAPPLSLANLFGEDGSLSPSPADSRPAGP 60  
 QY 61 GDGRPNLMMKFOGAFKRVGNPIDLLESTIYESSVVPKKAAMDLSFDYGTGRHSNDN 120  
 Db 61 GDGRPNLMMKFOGAFKRVGNPIDLLESTIYESSVVPKKAAMDLSFDYGTGRHSNDN 120  
 QY 121 KRMKKITIEKOPQSKAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLPFLTHKKRL 180  
 Db 121 KRMKKITIEKOPQSKAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLPFLTHKKRL 180  
 QY 181 TDEEFREPSGTGTCPLKALLNLSNGRNDTIPVLLDIARTGNMFEFINSPPRODIYYRGOT 240  
 Db 181 TDEEFREPSGTGTCPLKALLNLSNGRNDTIPVLLDIARTGNMFEFINSPPRODIYYRGOT 240

Db 181 TDEEFREPSGTGTCPLKALLNLSNGRNDTIPVLLDIARTGNMFEFINSPPRODIYYRGOT 240  
 QY 241 ALHIAIERCKHYVELLVAGADVAHQAGRFQPPQDEGGYFFFGSLPLSLACTQPHI 300  
 Db 241 ALHIAIERCKHYVELLVAGADVAHQAGRFQPPQDEGGYFFFGSLPLSLACTQPHI 300  
 QY 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTENTKFTVKMTDLLLKKCARLPDS 360  
 Db 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTENTKFTVKMTDLLLKKCARLPDS 360  
 QY 361 NLEAVANNNDGSLPMAAAKTGKIGIFOHIIIRREVTEDETRHSRKFKDMAVGVVSSLYD 420  
 Db 361 NLEAVANNNDGSLPMAAAKTGKIGIFOHIIIRREVTEDETRHSRKFKDMAVGVVSSLYD 420  
 QY 421 LSSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSFYINVSYL 480  
 Db 421 LSSLDTCGGEASVLEILVYNSKIENHMLAVEPINELLRDWRKKGAVSFYINVSYL 480  
 QY 481 AMVIFTLTAAYOPLGEGTPPYRTTYDYRLAGEVITLFTGVLFPTNKKDLPMKKCPGV 540  
 Db 481 AMVIFTLTAAYOPLGEGTPPYRTTYDYRLAGEVITLFTGVLFPTNKKDLPMKKCPGV 540  
 QY 541 NSLFDGSPQLYFYISVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600  
 Db 541 NSLFDGSPQLYFYISVIVSAALYLAGIEAYLAVMFALVGMNMLYFTRGKLTG 600  
 QY 601 TYSIMIOKILFKDLRFELLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660  
 Db 601 TYSIMIOKILFKDLRFELLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660  
 QY 661 RDSFTFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720  
 Db 661 RDSFTFSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIIILFTVLLNMLIALMGE 720  
 QY 721 TVGVSKESKSHIWKLO 736  
 Db 721 TVGVSKESKSHIWKLO 736

## RESULT 15

US-09-932-165-1477  
 ; Sequence 1477, Application US/09932165  
 ; Publication No. US20030134784A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: CHALITRA-ELD, PIA M.  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: SAFERAN, DOUGLAS  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: HUBERT, RENNE  
 ; APPLICANT: GE, WANGMAO  
 ; TITLE OF INVENTION: NOCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
 ; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
 ; FILE REFERENCE: DETECTION OF CANCER  
 ; CURRENT APPLICATION NUMBER: US/09/932,165  
 ; CURRENT FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: 60/226,329  
 ; NUMBER OF SEQ ID NOS: 1508  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1477  
 ; LENGTH: 963  
 ; TYPE: PRT  
 ; ORGANISM: Unknown Organism  
 ; FEATURES:  
 ; OTHER INFORMATION: Description of Unknown Organism: CatF2E11  
 ; OTHER INFORMATION: nucleotide sequence  
 US-09-932-165-1477

Query Match 98.8%; Score 3810; DB 10; Length 963;

Best Local Similarity 99.6%; Pred. No. 2.3e-303;  
Matches 733; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MADSEGPAGGAEVAELPGDESGTPGGAPPLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 93 MADSEGPAGGAEVAELPGDESGTPGGAPPLSSLANLFEGEDGSLSPSPADASRPAGP 152
QY 61 GGRPRLRMKFGQAPRKGVNPIDLESTLYESSVPGPKKAPMDSLFDYGYRRHSSDN 120
DB 153 GGRPRLRMKFGQAPRKGVNPIDLESTLYESSVPGPKKAPMDSLFDYGYRRHSSDN 212
QY 121 KEMRKXIIIEKOPQSPKAPAPPEPILKVENRPILEDIVSRGSTADLDGLPELLTHKKRL 180
DB 213 KEMRKXIIIEKOPQSPKAPAPPEPILKVENRPILEDIVSRGSTADLDGLPELLTHKKRL 272
QY 181 TDEEREPSTGKTCLEPKALINLSNGNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
DB 273 TDEEREPSTGKTCLEPKALINLSNGNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 332
QY 241 ALHIAIERRCKHYVELLVAGADVHAQAGRFQPKDEGGYFYFGEPLSLAACTNQPHI 300
DB 333 ALHIAIERRCKHYVELLVAGADVHAQAGRFQPKDEGGYFYFGEPLSLAACTNQPHI 392
QY 301 VNYLTENPKKADMRQRDSRGNTVAHALVAIADNTRENTKPYTKMYDILLKCARLPDS 360
DB 393 VNYLTENPKKADMRQRDSRGNTVAHALVAIADNTRENTKPYTKMYDILLKCARLPDS 452
QY 361 NLEAVINNDGLSLPMAAATGKIGIHOHIIREVTEDETRHLSRKFKDWAYGVPYSSLYD 420
DB 453 NLEAVINNDGLSLPMAAATGKIGIHOHIIREVTEDETRHLSRKFKDWAYGVPYSSLYD 512
QY 421 LSLDTCGEEASYLEILVYNSKIENRHEMLAVEPINELRDKWRKFGAVSFYINVSYLQ 480
DB 513 LSLDTCGEEASYLEILVYNSKIENRHEMLAVEPINELRDKWRKFGAVSFYINVSYLQ 572
QY 481 AMVIFTLTAAYOPLBGTPPYRPTVDYRLAGEVITLFTGVLPFTNIDKLFMKKCPGV 540
DB 573 AMVIFTLTAAYOPLBGTPPYRPTVDYRLAGEVITLFTGVLPFTNIDKLFMKKCPGV 632
QY 541 NSLPIFGSPQLLYFYISVLVIVSAALYLAGIEAYLAMVAFALVGMWMLYFTRGLKLTG 600
DB 633 NSLPIFGSPQLLYFYISVLVIVSAALYLAGIEAYLAMVAFALVGMWMLYFTRGLKLTG 692
QY 601 TYSIMIOKILFKDLFRFLVYLLFEMIGYASALVSLNPCANMKVCNEDQTNCTVPTYPSC 660
DB 693 TYSIMIOKILFKDLFRFLVYLLFEMIGYASALVSLNPCANMKVCNEDQTNCTVPTYPSC 752
QY 661 RDETEPSTFLLDLEKLTIGMDLEMLSTYYPVFIIILVYIIILTFVLLINMLIALMGE 720
DB 753 RDETEPSTFLLDLEKLTIGMDLEMLSTYYPVFIIILVYIIILTFVLLINMLIALMGE 812
QY 721 TVGVSKESKHIWKLQ 736
DB 813 TVGVSKESKHIWKLQ 828
```

Search completed: December 2, 2004, 22:39:18  
Job time : 152 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 2, 2004, 22:17:36 ; Search time 44 Seconds

(without alignments)  
1622.565 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSEGPRAQGEVALLPG.....GVSKSKHKLWKGSRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1579.5	40.9	838	2	T09054
2	1551.5	40.2	839	2	JC7621
3	736.5	19.1	727	2	JC7796
4	724.5	18.8	725	2	JC7531
5	719	18.6	723	2	JC7795
6	473.5	12.3	937	2	T37241
7	473.5	12.3	957	2	D88651
8	435.5	11.3	900	2	T33026
9	313.5	8.1	790	2	T20312
10	278	7.2	519	2	T24772
11	204.5	5.3	1188	2	T19552
12	188	4.9	828	2	JC5807
13	145.5	3.8	1124	2	JH0588
14	138.5	3.6	810	2	I38361
15	137	3.6	616	2	T00894
16	137	3.6	1765	2	T42388
17	136.5	3.5	683	2	A85044
18	136	3.5	2352	2	J30201
19	134	3.5	1275	2	JU0092
20	133	3.4	481	2	T23729
21	132	3.4	1274	2	JN0015
22	131.5	3.4	642	2	S88154
23	130.5	3.4	652	2	D85044
24	129.5	3.4	608	2	G02640
25	129	3.3	823	2	S44873
26	127.5	3.3	4377	2	A55575
27	126.5	3.3	643	2	D86167
28	126.5	3.3	2471	2	A49128
29	126	3.3	2212	2	A41098

30	125.5	3.3	934	1	H71274	probable ankyrin -
31	125.5	3.3	2529	2	B64635	toxin-like outer m
32	125	3.2	1957	2	S68453	sodium channel pro
33	124	3.2	793	2	S68238	trp-1 protein - nu
34	123.5	3.2	968	2	A37867	transcription fact
35	123	3.2	751	2	F85043	hypothetical prote
36	123	3.2	2531	2	T31070	notch homolog - se
37	121	3.1	488	2	JC7995	transient receptor
38	121	3.1	1549	2	T13940	ankyrin - fruit fl
39	120.5	3.1	397	2	T46445	hypothetical prote
40	120.5	3.1	573	2	D86464	Flg22.13 protein
41	120.5	3.1	664	2	A56695	notch2 protein hom
42	120	3.1	633	2	T27499	hypothetical prote
43	119.5	3.1	574	2	T47566	hypothetical prote
44	119	3.1	1765	2	T42714	ankyrin 3' splice
45	119	3.1	1940	2	T42715	ankyrin 3' splice

## ALIGNMENTS

## RESULT 1

T09054  
capsaicin receptor - rat  
N.Alternate names: vanilloid receptor subtype 1  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C.Accession: T09054  
R.Caterina, M.J.; Schumacher, M.A.; Tomlinaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D.  
Nature 389, 816-824, 1997  
A.Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.  
A.Reference number: Z16539; MUID:98007969; PMID:9349813  
A.Accession: T09054  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-838 <CAT>  
A.Cross-references: UNIPROT:O35433; EMBL:AF029310; NID:G2570932; PIDN:AA053398.1; PID:G  
A.Experimental source: dorsal root ganglion  
C.Keywords: ion channel; receptor

Query Match	40.9%	Score	1579.5;	DB 2;	Length	838;
Best Local Similarity	44.6%	Pred. No.	1.1e-103;			
Matches	338;	Conservative	129;	Mismatches	193;	Indels 97; Gaps 16;
QY	16	AELEPDESGTGGG-----	APPLSLANLFEDEGDSISPPADA	54		
DB	5	ASLSSESEKSPQENSCLDPPDRDNCKPPVKKPHITFRSRTRLF-GKGDSEASPLDC	63			
QY	55	SRPAGPGDGRPNLRMKFGQAFKGVFN-PIDLESTLYESSVDPGPKKAPMDSLFYGTY	113			
DB	64	FYBEG-----GLASCPITVSSVL-----TIQRPGDG-----ASV	94			
QY	114	RHHSNDKRMKRIIEKOPSPKAPAPOPPPILVFNPNPILFDIVSRGSTDLGLPFL	173			
DB	95	RPSQDS-----VSAGEKPP--FLYRRRSIFDVAQSCCELSLPLFL	136			
QY	174	LTHKKRLDEERFREPSTGKTCIPKALNLSGRBDTIPVLDIERTGNMBEPTNSPPRD	233			
DB	137	QRSKKRLTDSFKQPEFGKTCILKAMLNHNGDNTIALLDVARKDTSLOPFVNASYTD	196			
QY	234	IYRQGTALTAIERRCKHYVELLVAQADVAHAQARGFPOPKDGGYFEGELPLSLAA	293			
DB	197	SYRGQPLTAIRIAIRRMNTLVTLLVENGADVOAANGDFPKTKGRPGFYGELEPLSLAA	256			
QY	294	CTNCPHYVNTENPHKKAKMRDQSGNVTYLAHALVAIDNTRENTKVTYTDILLKLC	353			
DB	257	CTNGLAIVKFLIQQNSWQPADISARDVGNVTYLAHALVEVADVTNTKFTVSYMYEILLIG	316			
QY	354	ARLPDSNLZAVLANNDSPLPMAAKTGKIGIPQHIRREVTDDTRHLSKPKOMAYGP	413			
DB	317	AKHPTLKEBITNRKGIITPLALAASSGKIGVALYIQRHEHECHLSKFTFEMAYGP	376			
QY	414	VYSLVYDLSIDTCGEASVLEILVY--NSKIENHEMLAVEPINELLDRKRRKGAVSFY	472			

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Db      377 VHSSTYDLSCTDTC-EKNSVLEVIAYSSSETPNRHDMVLVEPLNLQDQKMRPFVKRIEY 435
Qy      473 INWVSILCAMVITFTLTANYQIPLEGTPPYRTTY-DYLRAGEVITLFTGVLEFFTNIKD 531
Db      436 NFNFYCCLYMIFLTAAYYRPEGLPEYKLNKTVSDYFVTEBILLSVSGGVFFRGIO- 494
Qy      532 LFMKCPGVNSLFIIGSFLIYFISVLYVISAALYLAGIEAVLYAMVFAVLGMNNALY 591
Db      495 YELQGRPSLSKSLFVDSYSILFVQSLFPLVSVLYFSGRKEVYASWVPSILMGMNTNLY 554
Qy      592 FTGRLKLTGTYSIMTOKILFKDLFRLVLYLLFMIGVASALVSLNPCANMKVCNEDQTN 651
Db      555 YTRGFQMGITVAMVEMKMLRDLCRFMFYLVFLFSGFAVVTLLI-----EDGKN 604
Qy      652 CLVP---LYPSGRDS-----EFSTFLDLFPLTIGMGDLEMLSTKYVVFPIIL 699
Db      605 NSLPMSSTPHKRGSGCKRGNSYNSLYST-CLBLEFPTIGMGDLFTENYDKAVFIILL 663
Qy      700 VTYIILTEVILNMLIALMGFTVGVSKESKHIWKLO 736
Db      664 LAVVILITLILNMLIALMGFTVKNKAQSKNIWKLO 700

RESULT 2
JC7621
capsaicin receptor, VR1 - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07621
R/Corr/Right, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A/Title: The tissue distribution and functional characterization of human VR1.
A/Reference number: J07621; MIMD:21139751; PMID:11243859
A/Comments: Dorsal root ganglia
A/Accession: J07621
A/Molecule type: mRNA
A/Residues: 1-839 <COR>
A/Cross-references: UNIPROT:Q9H304; GB:AF196175
C/Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
ligand integrative activation by several noxious stimuli, and plays an important role in in
C/Genetics:
A/Map position: 17p13
C/Keywords: transmembrane protein
F/201-233/Domain: ankyrin #status predicted <ANK1>
F/248-280/Domain: ankyrin #status predicted <ANK2>
F/333-365/Domain: ankyrin #status predicted <ANK3>
F/477-495/Domain: transmembrane #status predicted <TM1>
F/508-531/Domain: transmembrane #status predicted <TM2>
F/543-569/Domain: transmembrane #status predicted <TM3>
F/578-597/Domain: transmembrane #status predicted <TM5>
F/624-644/Region: pore loop #status predicted
F/656-684/Domain: transmembrane #status predicted <TM6>

Query Match 40.2%; Score 1551.5; DB 2; Length 839;
Best Local Similarity 44.4%; Pred. No. 1.1e-101;
Matches 320; Conservative 138; Mismatches 189; Indels 74; Gaps 12;

Qy      49 PSPADSRPAGPDGRPNL-----RKMFQG-----AFKGVNPPIDLES--TYESSV 95
Db      22 PDLIDGDPNRPAPKQSLSTAKSRTRLFGKGSSEAFVPCHEBGELEDSCTITVSPV 81
Qy      96 V-----PGKKAPMOSLFDYGYRHHSSDNKMKRKKIIEKQSPKAPAPQPPILKVF 149
Db      82 ITIQRPDGGTGAKL-----LSQDSVAASIEKILKLV 113
Qy      150 NRPIFLDIVSRGSTADLDGLPLLTTHKKRLTDEEPREPSTGKTCLEPKALLNSNGNDT 209
Db      114 DRKSIEEAVAGNNQCODESLFLQSKKILTDNEFDPEFGTKCLLKAMLNLDHGQNTT 173
Qy      210 IPVLIDIAERTGMREFINSPPRDIYRGQTALHIALIERCKHYVELLVAGQADVAAQAR 269

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Db      174 IPLLEIARQDSDLSKEIENASVYDSYVQGTALHIALIERRNALVTLLVENADVAQAAN 233
Qy      270 GRFPQKDEGGVYFYGELPLSLAACTNQPHLYNVTLENPHKKADARPODSRNTVLAHV 329
Db      224 GDFPKTKGRPGFTYGEPLSLAACTNOLGIVKFLQNSWQADISADSVNTVLAHV 293
Qy      330 ALADNTRENTKVTMYDILLKCARLPDSNLEAVLNNDGISPLMMAAKTKIGI FOHI 389
Db      294 EVADNTADNTKVTSMYNEIILMLGAKLHPTLLEETLTKKKGWTPALAACTKIGVLAVI 353
Qy      390 IRRVTDERTLRSKFDMAAGPYSSLYDLSLDTGSEBSVLEILVY-NSKLENRHE 448
Db      354 LQRELOEPCRHLSKRFEMAGPVHSSLYDLSCTDC-EKNSVLEVIAYSSSETPNRHD 412
Qy      449 MAAVPEIHELADKRRKGAVSFYINWVSYLCAWVITLTAYYOPLEGTPPYRTTYDY 508
Db      413 MLVPEPLRLQDKXDRFVKRIEFYFNFLVYCLMIIFTMAAYRPPVDGLPPEKMEIGDY 472
Qy      509 IRLAGEVITLFTGVLEFFFTNIKDLMKCPGVNSLFIIGSFLIYFISVLYVISAALYL 568
Db      473 FRYTGEIILSVLGAVYFFRGIO-YELQGRPSLSKSLFVDSYSMLFPLQSLFMLATVLYF 531
Qy      569 AGIEAVLYAMVFAVLGMNNALYFTRGLKLTGTYSIMOKILFKDLFRLVLYLLFMIGY 628
Db      532 SHLKEVASMVSLSLGMNTMLYTRGFQMGITVAMVEMKMLRDLCRFMFYIYVFLRGF 591
Qy      629 ASALVSLNPCANMKVCNEDQTNCTVPTY-----PSCRDSST-----FSTFLIDLFK 675
Db      592 STRAVTLLI-----EDGKNDSLPSSESTSHRRGPAACRPDPSYNSLYST-CLBLEFK 640
Qy      676 LTIGMGDLEMLSTYKPVVFIILTYITLTVLLNMLIALMGFTVGVSKESKHIWKLO 735
Db      641 FTIGMGDLEFTENYDFKAVFIILLAVYITLILNMLIALMGFTVKNKAQSKNIWKLO 700
Qy      736 Q 736
Db      701 Q 701

```

## RESULT 3

JC7796

epithelial calcium channel 2, ECAC2 - mouse

N/Alternate names: calcium T1; CAT1

C/Species: Mus musculus (house mouse)

C/Date: 02-Apr-2002 #sequence\_revision 17-May-2002 #text\_change 09-Jul-2004

C/Accession: J07796

R/Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.

Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001

A/Title: Gene structure and regulation of the murine epithelial calcium channels ECAC1 a

A/Reference number: J07795

A/Accession: J07796

A/Molecule type: DNA

A/Residues: 1-727 &lt;WEB&gt;

A/Cross-references: UNIPROT:Q91WD2; GB:AF336378

C/Comment: This calcium channel plays an important role in active transcellular calcium

relevant for in vivo calcium homeostasis.

C/Genetics:

A/Map position: 6

A/Introns: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; 428/2; 483/3; 50

C/Keywords: calcium channel

Query Match 19.1%; Score 736.5; DB 2; Length 727;  
 Best Local Similarity 33.3%; Pred. No. 4.4e-44;  
 Matches 196; Conservative 101; Mismatches 193; Indels 99; Gaps 21;

```

Qy      183 EEPREPGTGTCPKXLL--NLNGRNDTIPVLDIAERGNRREFINSPPRDIYRGQT 240
Db      71 EYHQRGMGFTALHIALYDNL-----EAMVMEAAP-----ELVFEMTSELHGGOT 119
Qy      241 ALHAIATERCKHYVELLVAGQADVAAQARFPQKDEGGVYFYGELPLSLAACTNQPHI 300

```

```

Db      120 ALHIAVINQNVNLVRLALLARGASVSARATGVSFHHKPH-NLIYGEHPLSFAACVGSSEI 178
Qy      301 VNYLTENPKKADMRQDSRGNTVLAHALVADNTEENTKFTYKMYDILL-----LKC 353
Db      179 VKLLIEH---GADIRADQSLGNTVHLITL-----LQPNKTFACQMNLLSLDGGDHLC- 229
Qy      354 ARLPDPSNLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVTDETRHLSRKFKWYAGP 413
Db      230 -----SLELVPNNQGLTFPKLAGVEGNIYVHGHLMOCK-----RKHIIQWYGP 271
Qy      414 VYSLSYDSSLDTCGEASVLELIVYNSKIENHEMLAVPINELRDQKRFAGVAFYI 473
Db      272 LNSTLITLDEIDSSGDSGLLELIVTKKREAR-QILDDTPVKEISLWKMKRGREYFCV 330
Qy      474 NVVSYLCAMVITFLTAAYQPLE-----GTPP-----YPRRTVDYRLAGEVI 516
Db      331 LGALIVLYLIICTMCCVYRPLKERTNKRTPNDNTLMQCKLQEAIVTPEDDLRLVGEIV 390
Qy      517 TLTGVLFFFTNLIKDLFMKKCPGVNSLF-----IDGSQQLLYPIYSVLYVISAALYLAGIE 572
Db      391 SIIVGANIIILLVELPIDFRL---GVTRFFQGTILGSPFHVILITVAFMVLVTVMRLTND 447
Qy      573 AILAVWVPLVYGWNAALYTRGLKLTGYSTIMQKILFKDLFRFLVYLLEFVIGASAL 632
Db      448 GEVWPMSFALVIGWCVWYFARGFQMLGFTTMIQKMFQDLRFQCLMAVVLIGFASAF 507
Qy      633 VSLNLCAMKVCNEDQTNQ-TVPTPSCDSETFSTFLDLFKLTITGNG---DLEMIS 687
Db      508 YIIFQ-----TEPDELGHFYDYPMA---LFTSF--ELF-LTIIDGPANYVDL-- 550
Qy      688 STEYVVFILLVLYIILTFVLLNMLALMGETVQVSKSHIKLQ 736
Db      551 ----PMSVGYTAAPAIATLMLNLMLMGDTHWRVHERDELWRAQ 595

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RESULT 4
JC7531
Calcium transport protein, Cat1 - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: JC7531
R/Peng, J.B.; Chen, X.; Berger, U.V.; Wieremowicz, S.; Morton, C.C.; Vassilev, P.M.; Brown
Biochem. Biophys. Res. Commun. 278, 326-332, 2000
A/Title: Human calcium transport protein Cat1.
A/Reference number: JC7531; MUID:20551480; PMID:11097838
A/Accession: JC7531
A:Molecule type: mRNA
A:Residues: 1-725 <PEN>
A:Cross-references: UNIPROT:Q9H296; GB:AF304463
C/Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular c
line and kidney.
C/Genetics:
A:Gene: Cat1
A:Map position: 7q33-34
C/Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

```

```

Query Match      18.8%; Score 724.5; DB 2; Length 725;
Best Local Similarity 32.3%; Pred. No. 3,1e-43;
Matches 198; Conservative 99; Mismatches 218; Indels 87; Gaps 20;

Qy      171 PFLTHK-----KELTDEFR--EPSTGKTLPKALL--NLSGRNDTIPVLLDIA 217
Db      48 PILLAKDNVQALNKLKYEDECKVHHRGAMGETALHIALYDNL-----EAMVIMEAA 102
Qy      218 ERKGNMREFFINSPPROLYYAGQTLAHLAIERCKHYVELVAQADVHAQARGFPQPKD 277
Db      103 P-----ELVFEPTSTSELVYGQTLAHLAVNQNMLVRLALARAASVSARATGAFR-RS 155
Qy      278 EGGVFGELPLSLAAGCTNCPHYVNTENPHKKADMRQDSRGNTVLAHALVADNTE 337
Db      156 PCNLIYGEHPLSFAACVGSSEIYVLLIEH---GADIRADQSLGNTVHLITL-----LQ 207
Qy      338 NTKFVTNMYDILLKCARLPDPSNLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVTDE 397

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Db      208 NTKFACQWYNLLSYDRHGHLLQPLDLVPHGGLTFPKLAGVEGNTVMFOHLMCK----- 262
Qy      398 DTRHLSRKFKDWAGPVVYSLSYDSSLDTCGEASVLELIVYNSKIENHEMLAVPINE 457
Db      263 -----RKHIIQWYGPYFCGLAIVLYLIICTMCCVYRPLKERTNKRTPNDNTLMQCKLQ 315
Qy      458 ILDRKMRKRGAVSFYINVSYLCAVITFLTAAYQPLE-----GTPP-----Y 500
Db      316 LVSLMKRGYRPFQCLGALIVLYLIICTMCCVYRPLKERTNKRTPNDNTLMQCKLQ 375
Qy      501 PYRTVDYRLAGEVITLFTGVLFFFTNLIKDLFMKKCPGVNSLF-----IDGSQQLLYPIY 556
Db      376 AYMTPEKDRILVGEIVTVGALIIILLVEPDIFFRM---GVTRFFQGTILGSPFHVILITY 432
Qy      557 SVLYVISAALYLAGIEAVLAVWVPLVYGWNAALYTRGLKLTGYSTIMQKILFKDLFR 616
Db      433 AFVVLTVWVWRLISASGEVWPMFALVIGWCVWYFARGFQMLGFTTMIQKMFQDLRF 492
Qy      617 FLVYLLEFVIGASALVSLNLCAMKVCNEDQTNQ-TVPTPSCDSETFSTFLDLFK 675
Db      493 FCLMAVVLIGFASAFYIIFQ-----TEPDELGHFYDYPMA---LFTSF--ELF-- 537
Qy      676 LITGMDLEMLSTKTPVFIILVLYIILTFVLLNMLALMGETVQVSKSHIKLQ 735
Db      538 LTIIDGPANY--NVDLPFYISITYAFALITLMLNLMLMGDTHWRVHERDELWRA 595
Qy      736 Q 736
Db      596 Q 596

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RESULT 5
JC7795
epithelial calcium channel 1, ECaC1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C/Accession: JC7795
R/Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A/Title: Gene structure and regulation of the murine epithelial calcium channels ECaC1
A/Reference number: JC7795
A/Accession: JC7795
A:Molecule type: DNA
A:Residues: 1-723 <WEB>
A:Cross-references: GB:AF336378
C/Comment: This calcium channel plays an important role in active transcellular calcu
relevant for in vivo calcium homeostasis.
C/Genetics:
A:Gene: ECaC1
A:Map position: 6
A/Intons: 37/2; 70/1; 111/1; 157/1; 190/1; 247/3; 296/3; 367/3; 396/3; 422/2; 477/3;
C/Keywords: calcium channel

```

```

Query Match      18.6%; Score 719; DB 2; Length 723;
Best Local Similarity 33.3%; Pred. No. 7.6e-43;
Matches 201; Conservative 100; Mismatches 198; Indels 104; Gaps 23;

Qy      173 LITHKKRLNDE--EPRE-PSGKTLCPKALL--NLSGRNDTIPVLLD-----IABRTGN 222
Db      52 MCTLKQLQHDQNCDFRQALGETALHVALYDNL-----DAIMTMEAPLYVTEST-- 104
Qy      223 MREFFINSPPROLYYAGQTLAHLAIERCKHYVELVAQADVHAQARGFPQPKDEGGYF 282
Db      105 ----LCEPF-----VGQTLAHLAVNQNMLVRLALARAASVSARATGSAFH-RSSHNL 154
Qy      283 YGSELPLSLAAGCTNCPHYVNTENPHKKADMRQDSRGNTVLAHALVADNTEENTKFTY 342
Db      155 YGEHPLSFAACVGSSEIYVLLIEH---GADIRADQSLGNTVHLITL-----LQPNKTF 206
Qy      343 TKMYDILL-----LKCARLPDPSNLEAVLNNDGSLPLMMAAKTKIGIFQHIIRREVT 395
Db      207 CQMNLLSLDGGDHLC-----SLELVPNNQGLTFPKLAGVEGNTVMFOHLMCK--- 255

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QY 396 DEDTRHLSKFKKDMAYGVVSYLNDYSSLDUPCGEASLELLVYNSKILENHEMLAVERPI 455
Db 256 -----RKQIOWSFGBLTSSLDYLTETDIDSGEELSLELVSSKCKEAR-QILQCTPV 306
QY 456 NELLDRKMRKFGVASFYINNVSYLCAMVIFTLTAYQPL-----EGTP 498
Db 307 KEVSLAKKKKQGGPFCILGALYIFYWCFTTCCYRLKRDNRKTHVRDNTIMEQSL 366
QY 499 PYPRTTYDYIRLAGEVITLFTGVLFPPFTNIKDLFMKKCPGVNSLF---IDGSFOLLVF 554
Db 367 QEAVYTYODKRLVGEELVTYIGAVITLLEIPDR--VGASRYFGQTVLGGPETHVILI 423
QY 555 IYSLVIVYSALTYLAGIEAYLAWVFALVCGMNAHYTRGILKLTGYTSIMIOKILFDL 614
Db 424 TYASIVLITMTAMRLTNNGVEVPMWMAVLQWCSYMFARFGOMLGPFTIMIOKIMFGDL 483
QY 615 FRFLVLYLTFMIGVASALVSLNCPANKVCNEDQINC-TVPTPSCDSSTFSTFLLD 673
Db 484 LRFQWLANAMVILGFSASAFYIIIFQ-----TEDEBNIGERSDYPFTA---MFSTP--EL 529
QY 674 FKLATIGMGDLEMLSSTKXYPVVFILLYVITLFTVLLNMLIALMGETVQGVSKESKIHV 733
Db 530 F-LTIIDGPANY--RVDPFPMYSVTYATFALITLMLNLFLAMGDIHMYVAGERDEW 586
QY 734 KLQ 736
Db 587 RAQ 589

```

## RESULT 6

T37241  
olfactory channel protein osm-9 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: J37241  
R:Colbert, H.A.; Smith, T.L.; Bargmann, C.I.  
J. Neurosci. 17, 8259-8269, 1997  
A:Title: OSM-9, A novel protein with structural similarity to channels, is required for  
A:Reference number: J21639; MUID:97477445; PMID:9334401  
A:Accession: T37241  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-937 <COL>  
A:Cross-references: UNIPROT:O17469; EMBL:AF031408; NID:g2642589; PIDD:AA87064.1; PID:G2642589  
C:Genetics:  
A:Gene: osm-9  
A:Map position: IV  
A:Keywords: transmembrane protein

Query Match	12.3%	Score 473.5	DB 2	Length 937
Best Local Similarity	27.1%	Pred. No. 2.6e-25		
Matches 149	Conservative 90	Mismatches 213	Indels 97	Gaps 17

  

QY	233	DIYR---	GOTALHAI	IERCKHYV	LLVAQADV	HAQARPRDPK-----	DEG	279	
Db	163	DIYLGDEQ	FQFOSALH	IVDDDEY	VSLLNSK	ADVNARACGNF	PEDEPK	ITNKITDYQ 222	
QY	280	GVEYFGE	LPLSLA	CTQPHIV	NYLTFE--	NPHKAMR	RODSKGN	VLAVALADNR 336	
Db	223	GVAVYGE	YFLAPAAC	FENKOI	YDILLIQ	FANPN-----	LQDSGN	ITIMCV----- 269	
QY	337	ENTKPY	KMTDL	LLILKCAR	LFPDSN	LEAVLN	NDGLSP	IMAAATGKIGIPOHIIREEVTD 396	
Db	270	--INYS	SMTSYA	RRHAK--	PAD--	PHVNHG	FPTLTAT	KIGRKOIFEEMLE----- 318	
QY	397	EDTRHLS	RKKEDMA	YGVYS	SLYDLS	SLDTCCGE	EAASY----	LEILVNSKTE	NRHEWLAIV 452
Db	319	-----	IMKYE	FNRF	SDMTCS	AAPI	NLTLDIT	IQPDGS	INYSALMTVINSGTSPHIDMIGS 372
QY	453	EPINEL	LIDPKR	KFGAVS	FIYNVSY	ICAMVIT	LINAYO	PLP	EGTPPYRTTV--DYL 509
Db	373	EVIO	RLADCM	KFAQR	KLIER	VLLIV	LOVIT	ITS	IVVIRPTE--LPRLMEDPOWDYI 430

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QY 510 RAGGVITLFTGVLF-----PFTNKKDLMKKCPQVNSLFDIGSPQLLY 553
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 431 RTACGLLITLINCITFFVGVQOGLSEITQGMKGITRLNRKTKTPAKRVFCIANLFT----- 482
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 554 FLYSVLVIVSAALYIAGIBAYIAVAVFALVIGMMNALYFTRGKLTGTYSIMIÖKTLFKD 613
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 483 ---ALICPFRIMKGEIEE-ALFVFALPGSWIFILFFARSAKLTGPFQÖMITYSMIAGD 536
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 614 LERFLVLVLLFMIGYASALVSL-LNPPCANMKYCNÖDQNTC-----LVPPYPSRDBETFS 667
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 537 MIRPFIISALFIVASQVFFVGVGMÖDKÖKLEDTNPHACRISGYITTY-----NTPE 590
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 668 TFLLDLFLKLTIGMDLEMLSTKPYVVFLLLVTYIILFEVLLNLNLALMGFTYQÖVSK 727
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 591 EFTFLFLFRAMGÖGYDEBESCANYGALRKTLFVLVLMFVPMIMMINILMMGÖTYTTVLA 650
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 728 ESKHTWKQ 736
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 651 ÖAEKAMRQÖ 659
    ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

## RESULT 7

D88651  
protein B0212.5 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: D88651  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MUID:59069613; PMID:9851916  
A:Note: see websites genome.muc1i.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D88651  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-957 <SNO>  
A:Cross-references: UNIROT:O17465; GB:chr\_IV; PIDN:AAOC2569.1; PID:g2854148; GSPDB:GN00C  
C:Genetics:  
A:Gene: B0212.5  
A:Map position: 4

Query	Best Local Similarity	27.1%	Pred. No. 2.7e+25;	Matches 149;	Conservative 90;	Mismatches 213;	Indels 97;	Gaps 17
QY	233	DIYVR----	GQTALHAIATERCKHVELLVAGQADVHQAARGFRFQPK-----	DEG	279			
Db	166	DIVLGDQPGQSALHIAIVHDDYETVSLINSSKADVNARACGNFLPDEDFKLTNKTIDVQ	225					
QY	280	GYFFGELPLSLAAGCTNOPIVNTYTE--	NPHKADMRRODSRGNTVLAHALVAIADNTR	336				
Db	226	GYAYGYGYPLAFACFGNKIDYDLLIOFGANPN-----	LDDSFNTILHMCV-----	272				
QY	337	ENTKFTVKMDLLTLKCARLEFPDNLSEAVLINDGSLPLMAAKTGKIGFQHIIRREYTD	396					
Db	273	--IYSSSMYSYAVRHMVK--PAD--	PHVNHAGETPLTLATKLGKQKOFBEMLL----	321				
QY	397	EDTRHLRKFEDMAVGYVYSSLYDLSLDTCGEBAV--	LEILVYNSKLENRHMLAV	452				
Db	322	-----IMKVEFMRFSMDTCSAVPLNTLDIQLPQDSTNYDSALMTVINGSTPEHLMIGS	375					
QY	453	EPINELLIRDKRKKGAVSFYINVYSYLCAWVI	FTLTAYQPLEGTPPYRTTV--	DYL	509			
Db	376	EVILORLLADMKKFAQKRLIERLIVLLIVQLITLSIVVYIRPTE--	LPRLYMEDDPOMDYI	433				
QY	510	RLGGEVTLTFGVLF-----	FFNINIKLPMKKCGGVNSLFDGSGFOLLY	553				
Db	434	RTACEELLINCFIPFVGYYQOLGEIRTOGMRGYNLRNLKAPAKAVFIANLPL-----	485					
QY	554	FIVSVLVIVSAALYIAGIEAVLAWFEVLAIVGMNNALYFTRGLKLTGYYSIMIOKILEKD	613					

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Db      486 ----LTCIFRLMKHEIEE--ALFVFLPGSMWLELFPARSAXLGTGPFVQMIYSIMAGD 539
Qy      614 LRFLLVYLLEFMIGVASALVSL-TNP CANMKVCNDQNTC-----TVFPYSCRSSEFSS 667
      540 MRFALISAFLVSSQVFPYFGKMDAKOKIEDNPACRISGTYITVY-----NTP 593
Db      668 TFLDLFKLTIGMDLEMLSTKYPVFIILLVYIITFLVLLNMLTALMGETVGOVSK 727
Qy      594 EFTFLTFPASMGGDYEEFSCANYQALTKTLFVLVFMFVPMIMINILLAMGNTVTVYA 653
Db      728 ESKHMKQ 736
Qy      654 QAEKXMRQ 662

```

## RESULT 8

hypothetical protein T09A12.3 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T33026

R/Hawkins, J.; Fulton, B.; Gilliam, B.

submitted to the EMBL Data Library, February 1996

A/Description: The sequence of *C. elegans* cosmid T09A12.

A/Reference number: 221265

A/Accession: T33026

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-900 <HAM>

A/Cross-references: UNIPROT:O61220; EMBL:AF047660; PIDN:AMC04431.1; GSPDB:GN00022; CESP:

A/Experimental source: strain Bristol N2; clone T09A12

C/Genetics:

A/Gene: CESP:T09A12.3

A/Map position: 4

A/Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3; 82

Query Match 11.3%; Score 435.5; DB 2; Length 900;

Best Local Similarity 24.9%; Pred. No. 1.2e-22;

Matches 167; Conservative 99; Mismatches 231; Indels 173; Gaps 26;

```

Qy      189 STGTCTCPKALINISNGNDITPVLLDIAERTGMREINSFPRDIY---YRGQTALHI 244
Db      154 SMGFTTIGCCLLHMSDHNALVLTLDYLPKILN-----DIHISEDYFGSLPHQ 203
Qy      245 A-IERRCKHYVELVAQADVAHAQARGRFQPKDE-----GSGYF 282
Db      204 AIIITDCK-LVYKFLKLGADVNSKCYGAFCAADQKASRTSLSEHYVELSLKNTYTM 262
Qy      283 YFGEPLISLAACNPHIVNLTENPHKADMRQDSRGNTVLAHVAIADNRENTKTV 342
Db      263 YLGEVPLISFACTLNQPEFRLILA--FKANPNAQDTGNSVLMHCV-----IHENMAF 314
Qy      343 TKMTVDLLIKCARLEPPDSNLEAVINNDGLSPLMMAAKTGKIGIQTIRREVTDEDRHL 402
Db      315 K-----LALREG-----ASLRTV-NKOSLSPLTLAAKAKKEMDEILIEGDSV----- 358
Qy      403 SRKFKDVAAGPVYSLVDSLDTCGE-----EASVLEILVYNSKIENRHEMLAVEPIN 456
Db      359 -----NAYGDASTAIPACIDITINETGELNRSALSLVYQGYE--HELLDGLLD 410
Qy      457 ELRLDKRKFG---AVSEYINVSYLCAVIFTL-----TAYYQPLEG- 496
Db      411 TLLEAKNEAFKRMNIVSFTAFPLYICFVTAFLIRPIGFSTEMLTGEMINRYSEBPRGR 470
Qy      497 -----TPPYRPTVDYRLAGE---VI 516
Db      471 YGNKSTIQQKVPVINATSRGLVSEPSISQCHLNWDPIRPNAS--YIRLVEELPVI 528
Qy      517 TLFTGVLEFFTNIDLPFKKCPGVNSLF-IDGSFQLYFIYSVVIYSALYLAGIAYL 575
Db      529 GICGVPLDFRDIKRIKRWKMMVLTAPPAKITFTLYFLVAMIPRLACDLSPLVLYV 588

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Qy      576 --AVWFAVLGWMNALYFTREGLKLTGYYSIMIQILFKDLRFLLVYLLFMIGVASALV 633
      589 DNVLITVMIPTTHVLYLVCVIRRVGPFVLMVYIITATDIFRFLIIGIFLMGSGSS 648
Qy      634 SLNDC--AN-MKVCNDQNTC-----VPTPSC--RDETFSS----- 667
Db      649 LIFLSCREANVIXKLTIDQSEASESGSDNKRTLTROIASVDTAIVKNAVEFENVMQSPIE 708
Qy      668 ----TFLDLFKLTIGMDLEMLSTKYPVFIILLVYIITFLVLLNMLTALMG---E 720
Db      709 AFVFTLITGSEFVLYRNIALCPANLTMWIGKVFILFELFVSIMQFNMLAMTTRYE 768
Qy      721 TVGQVSKESK 730
Db      769 TIFQTGLEVK 778

```

## RESULT 9

T20312

hypothetical protein F28H7.10 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T20312; T21533

R/Matthews, P.

submitted to the EMBL Data Library, June 1996

A/Reference number: Z19255

A/Accession: T20312

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-790 <WII>

A/Cross-references: UNIPROT:P90784; EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN00023; CESP:F

A/Experimental source: clone D1054

R/Berks, M.

submitted to the EMBL Data Library, May 1996

A/Reference number: Z19435

A/Accession: T21533

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-790 <WII>

A/Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN00023; CESP:F28H7.10

A/Experimental source: clone F28H7

C/Genetics:

A/Gene: CESP:F28H7.10

A/Map position: 5

A/Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 6

Query Match 8.1%; Score 313.5; DB 2; Length 790;

Best Local Similarity 22.0%; Pred. No. 4.4e-14;

Matches 155; Conservative 94; Mismatches 209; Indels 245; Gaps 28;

```

Qy      152 PILFDIVSRGSTALDGLLPFLTHKKRL-----TDEEPR-----PSTGK 192
Db      109 PNILDEPDQO-AEMAQDL-----KRALKLDDGGKSGKSEKTRKRWWSVDERGSGE 161
Qy      193 TCEPKALINISNGNDITPVLLDIAERTGN-MREFINSFPRDIYRGQTALHAIERRCK 251
Db      162 NLALICLLQSGALHN-----LIARLINFPPLINDICVSEYGYGSLHAIIVQDA 214
Qy      252 HYVELVAQADVAHAQARGRFQPKDE-----GGFYGEPLS 290
Db      215 QFTSLIRLQADLNQRCYGAFFCADQKASRTDSLSEHVELTKNTNYTGSMTGEYPLS 274
Qy      291 LAACNPHIVNLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVTKVYDILL 350
Db      275 FALCMGQHDLPKMLLA--KKANISADDTNGNTLIR-LCVIHD--KK-DNL- 318
Qy      351 LKCARLEPPDSNLEA--VINNDGLSPLMMAATGKIGIQTIRREVTDEDRHL 405
Db      319 -----DAVLBAGNIRILANKONLVALTLAARLAK-----KTESIQHLE-- 356
Qy      406 FKMAAGPVYSLVDSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDWRK 465
Db      357 -----LMDGLLEQILDERKWA 372

```



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QY 466 FGAVSYINNVSYLCAMVIFLTLAYVOPLEGTPPYRTVD----- 507
| : : : : :
DB 373 YGRALMMSLILGIFFYCCFVCAMVLRPESATTEHLTRGRINDDBESTSTNGTNYLQWHA 432
QY 508 -----YLRAGEVITLFT---GVLFFPTNKKDL-----FMKKCKG 539
| : : : : :
DB 433 IDTOCHLMYASAMPWYHGFRLGCEIMTIVMLFOLLDFGDIRIRGFOKWFNFKAKFA 492
QY 540 VNSLFIDSGFOLLFYFYSVLVTSALVLAGIEAYLAV---MVFALVGMNNALEYTRG 595
| : : : : :
DB 493 --KLMFKGAF--LFIITISIPCLAGSFH---EFLITNTMAIISILVTOHFLIYVMA 544
QY 536 LKLTGTYSIMIOKILFKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVP 655
| : : : : :
DB 545 IFFVGFVLMVYTIATDLVRFAMYSIFLVGFSQGFYIFTSCE----- 589
QY 656 TTPSGRDSSTF-----STF-----LIDLKLTIGMDL---EMLSTKYPVF 695
| : : : : :
DB 590 -----RDSIALKIDPMGSEFNINMENPVDALLRTFTMTIGEPSVLYREMSACDNFMKM 644
QY 636 IILVYIILTFVLL--NMLIALMG---ETVGOVSKESKHIM 733
| : : : : :
DB 645 ICKLIFVIFETVYSILQFLLIAMMTKRYETIFLRKMKRQW 687

```

## RESULT 10

```

T24772
hypothetical protein t10b10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24772
R:Sim, M.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19934
A:Accession: T24772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-519 <WILL>
A:Cross-references: UNIPROT:Q22374; EMBL:Z72514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:TL
A:Experimental source: clone t10b10
C:Genetics:
A:Gene: CESP:T10B10.7
A:Map position: X
A:Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

```

```

Query Match 7.2%; Score 278; DB 2; Length 519;
Best Local Similarity 29.5%; Pred. No. 7.9e-12;
Matches 89; Conservative 36; Mismatches 115; Indels 62; Gaps 10;

```

```

QY 216 IABRTGNMKEEINSPF-RDIYR--GOTAIHAIERRCKHYVELVAQADVAQAQRF 272
| : : : : :
DB 161 VKQMTYRFPKIVNDIFLSEYYASVGLSPHQIIVNEDLEMYVFLCRKADVAHQRCYGSF 220
QY 273 FQPKDE-----GGYFVGEGLPLSLAAGTQNPPIVNYLTENPHKK 311
| : : : : :
DB 221 FCADDKASRTDSLEHEWDLVOSTKYTQGMWGEPLSPFACTNOYDCERLRA--MK 277
QY 312 ADKRDSRGNVVAHALVAIADNTRENTKVTQMYDLLLKCARLPDSNLEAVLNDDG 371
| : : : : :
DB 278 ADPNMDDTNGNTYLH-----LTVIHLPENFMALVAGANLH--VRNNLKI 321
QY 372 SPLMAAKTGKIGIFQHIIRREVTDERTRLSRKFKDMAYGPYSSLYDLSLDTGGE 430
| : : : : :
DB 322 TPLALAAARKKIIYDLILE--CDMDI-----SMRYGPVCKAKAYPLNDVDITNESD 370
QY 431 -----ASVLEIIVYNNKIEHREHMLAVEPINELRDKMRKREGAVSYINNVSYLCAMVF 485
| : : : : :
DB 371 GSINPNSVIANVVGKVD--HLEFPDGLIEVLSESKMETGKKQLFMSLAGITVFLAVF 428
QY 486 TL 487
DB 429 YL 430

```

## RESULT 11

```

T19552
hypothetical protein C29B6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jul-2004
C:Accession: T19552
R:Johnson, R.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19141
A:Accession: T19552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1188 <WILL>
A:Cross-references: UNIPROT:Q18297; EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C2
A:Experimental source: clone C29B6
C:Genetics:
A:Gene: CESP:C29B6.2
A:Map position: 4
A:Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

```

```

Query Match 5.3%; Score 204.5; DB 2; Length 1188;
Best Local Similarity 20.3%; Pred. No. 4.1e-06;
Matches 152; Conservative 98; Mismatches 250; Indels 247; Gaps 33;

```

```

QY 124 RKIIEKQSPKAPAPQPPILKVPNRPILFDIYSKSGTADLD-----GLPFLIT 175
| : : : : :
DB 418 RKKNKETERSAKSPRTNLRIVSDDVRYTVMVNRDQNTPMHIVASNGYLEMMQLQK 477
QY 176 HKKRLT---DEFPBSPGTCCLPKALLN-----SNG 205
| : : : : :
DB 478 HGASTITQVNEDEE-----TALHRAAIGVQLLEMDIRLLMDKEMNSALHIAARSG 529
QY 206 RNDTIPVLIDIAERTGNMKEEINSPFRIYRGQTAIHAIRCKHYVELLVAQADVA 265
| : : : : :
DB 530 HDATTKVLLD-----NGADKEAKNS-----YQ--KTPLOVAVDSGKLETQRLVAKAQILE 578
QY 266 AQ-----ARGFPQKQGGFYFGEGLPLSLAAGTQNPPIVNY 302
| : : : : :
DB 579 SSSDTKTVLHTAFAYGNEIVRYFLAEGVTIDRDEEGKYAD-----IAC----- 624
QY 303 YLTENPHKKADMR-----ODSRGNTVVAHALVAIAD-----NTRENTKE--VTKMYDYL 349
| : : : : :
DB 625 ---ENDHK--DVAKAFLETDQKMLMIPCDVIPLDGHRPVMKRTPTPRLITKPELA 679
QY 350 -----LLKCARLPDSNLEAVLNDDGLSLPMAAKTGKIGIFQHIIR-REVTDERTRLH 402
| : : : : :
DB 680 SFVMDKCIKSKBETDSTQSAVYNFEFLDDTYMMRCVSDDGEGQLGCKSAVDED----- 735
QY 403 SRKFKDMAYGPYSSLYDLSLDTGCEBASVLEIIVYN-----SKTENHEMLAVEPINE 457
| : : : : :
DB 736 ---FKLEKDAOSTASAYND-----RVYVHPLKIMADEKCH--LHNPILSK 776
QY 458 -LLRDKMRKGAVSFINNVSYLCAMVIFLTLAYVOPLEGTPPYRTVDYLRAGEVIL 516
| : : : : :
DB 777 ALLKTYMNLGRPMYFALPMYL--VFISLQVYVHTKA-----PYNWNNEESYVDS-- 828
QY 517 TLETGVLEFFTNIKDLFMKKCPGVNSLFTD-----GSFOLLY----- 533
| : : : : :
DB 829 -----YFDEN-----ETCCPQINTTKEDVWKKIITQILVAQQLIVEGQLORRKAAYL 875
QY 554 -----FYSVLYIV-----SAALYLAGIEAYLAVNVPALV---GMNNALEYTRGLK 598
| : : : : :
DB 876 VMNENMIDCFIYSTALITYVDFECSATGCVRONMOMIILALCTIFGMNINLMIKKMR 935
QY 599 TGTYSIMIOKILFKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVP 658
| : : : : :
DB 936 FGLFVVMFVDIV-KTFRRFPFVFLFLIASSSFFVIL----- 972
QY 659 SCRDSSTFTLIDLKLTIGM-----GD-----LEMLSTKYPVFIIILVYI 703
| : : : : :
DB 973 --QNRPEFTIFWSPKTTVMIMIGEFETGIFHGETTHAEKMGPAHRAVACALFEFFC 1030

```

QY 704 IITVLLINMLTALMGETVGVSKSK 730  
 Db 1031 IIMTILMLTALMGVLAVIDIKGVKAE 1057

## RESULT 12

trp3 protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 07-May-1999  
 C:Accession: J05807  
 R:Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.  
 Biochem. Biophys. Res. Commun. 240, 167-172, 1997  
 A:Title: Expression and characterization of a trp1 homolog from rat.  
 A:Reference number: J05807; MUID:98042538; PMID:9367904  
 A:Accession: J05807  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-828 <PRE>  
 A:Experimental source: brain  
 C:Comment: This protein participates in store-operated Ca2+ entry into cells.  
 C:Superfamily: TRPC3 protein

Query Match 4.9%; Score 188; DB 2; Length 828;  
 Best Local Similarity 20.6%; Pred. No. 3.6e-05;  
 Matches 137; Conservative 100; Mismatches 240; Indels 188; Gaps 31;

QY 210 IPVLIDIERGNGMREFFINSPRODIYRGOTAHIAIERCHYVELL-----VAQADV 264  
 Db 52 IPVRAKMLBSRTLN-VNC-----VDYGNALQAVNEHLEVTLLKKENLARIGDA 105  
 QY 265 -----HAQARGFPQP--KDEGFFYGE-----LPLSLAA 293  
 Db 106 LLMAISKGYRIVRAILSHPALAQQTSLPLERND--FYDEGTGTFSPDITPIIAA 163  
 QY 294 CTNOPIHYNYL-----TENPH--KKADMERQD-----SRGNTLHALVAADNT 335  
 Db 164 HCHKEVVAHLLILKGRTERPHDYLCRCADCAEQGLMTFSRSRINAYKASPGYLSLS 223  
 QY 336 RENTFVYKMYDILLKCARLEPPDSNLBAVLNNDGLSLPMAAKTKGIGF----- 386  
 Db 224 SEDVYLTALLESNEIAKLA-----NIKEPKND--YRKLQWQCFVGVVLDLCRDEEV 276  
 QY 387 QHIIREVTDEDTN-----LSR-----KFKDWAYGVYSSLYDLSLPTCGEASV- 433  
 Db 277 EAILNGDLESVEERHGHGASISRYVLAIKVEKKFVAVNCCQQLITTYGMLSGELAIX 336  
 QY 434 -LEILVNSKIENRHEMLAV-----EPINELRDKWRKFGAVSYINVSYLCAVTF 485  
 Db 337 CLVVLVVALAL-----PFLAIGWIAIPCRLKILRSPEMKFVAASFIL-----FLGLLVF 387  
 QY 486 TLTAAYGPLEGTTPPYRYTVDYRLAGEV--ITLFTGV-LFFPNIKDLMKKCPGVNSL 543  
 Db 388 NASRPF--EGITLLENITVDYPRKQIFRYVTQFTWTEMLIMVWVGMMWSEC--KEL 441  
 QY 544 FIDFSFOLLFYISYLVLS-----AALYLAGIEAYLA----- 576  
 Db 442 WLBPREFYQLMNVLDLSTIFIAFTARFLAFLCATGAQOQYVDSHVGESLVELTPREV 501  
 QY 577 -----VMPALVGMNALVYFTRGLKLTGYTSIMIQKILKDLF 615  
 Db 502 QYFTYARDKWLSPDOIISGLVYALVAVLSFSRIAYIIPANESFGPIQISLGRVY-KDIF 560  
 QY 616 RFLVYLLFMIGVASALVSLINPCANMKVCNEDQTCNCPYTPSCRDETFSTFLDLFK 675  
 Db 561 KFMVLFITGVFLAFMIGMFLYSYVGARV--DPAFTV-----EESFKTLFWSIFG 609  
 QY 676 LITIGMDLEMLST-KYFVVF-----ILVTYIILFVLLINMLALMGETVGVSKSK 729  
 Db 610 LS-----EVTSVLKKDHFENIGYLVGIYVNTVVVLLINMLALMINSYGEIIBDS 663  
 QY 730 KHIWK 734

Db 664 DVEMK 668

## RESULT 13

calmodulin-binding protein trp1 - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C:Accession: J05868  
 R:Phillips, A.M.; Bull, A.; Kelly, L.E.  
 Neuron 8, 631-642, 1992  
 A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with  
 A:Reference number: J05868; MUID:92232293; PMID:1314616  
 A:Accession: J05868  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1124 <PHI>  
 A:Cross-references: UNIPROT:P48994; GB:M88185; NID:G463057; PID:G158715  
 A:Experimental source: head  
 C:Genetics:  
 A:Gene: trp1  
 A:Cross-references: FlyBase:FBgn0005614  
 C:Superfamily: TRPC3 protein  
 C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein  
 F:341-362/Domain: transmembrane #status predicted <TM1>  
 F:374-396/Domain: transmembrane #status predicted <TM2>  
 F:462-479/Domain: transmembrane #status predicted <TM3>  
 F:512-533/Domain: transmembrane #status predicted <TM4>  
 F:549-572/Domain: transmembrane #status predicted <TM5>  
 F:643-668/Domain: transmembrane #status predicted <TM6>  
 F:710-727,809-825/Region: calmodulin binding #status predicted  
 F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 3.8%; Score 145.5; DB 2; Length 1124;  
 Best Local Similarity 19.3%; Pred. No. 0.057;  
 Matches 141; Conservative 99; Mismatches 237; Indels 253; Gaps 34;

QY 189 STGKTCPEKALNLSNGRNDITPVILD-----IATRG--NMREFFINSPREDIYR--- 237  
 Db 24 SVGGCCVPLGQPQ-----PILLEEKKTLAVERQDMVRRILOKALRHQININC 74  
 QY 238 -----GOTAHIAIERCHYVELLVAQAD-----VHAQ 267  
 Db 75 MDPLGRALTLAINENLWELLVWGVETKDALHAINAFVAVELLHHEBLIYKE 134  
 QY 268 ARGRFPQKDEGFFYFGEEL-PLSLACTNOPIHYNTEN-----PH----- 309  
 Db 135 GEPYSQWQVDINTAMFAPDITPMLAAHKNNFEILRLIDRGAAPVPHDRGCEECVR 194  
 QY 310 --KKADMERQDSRGN--TVLHALVAADNTRENTX-----VTQM-----YDL 348  
 Db 195 LTAEDSLRHSLSRNVITRALCPSLICITSDPSSTAAQLSWEILNALATQBECKSEYMD 254  
 QY 349 LILKCARLEFPD-----SNLBAVLNNDGLSPLMAAKTKGIGFQHIIRREVTDEDTN 400  
 Db 255 LRQCQKPAVDLADQTRTSNELAIIVVD--PQMSYEPG-----DRM 295  
 QY 401 HLSRKFQDMAYP---VYSSLYDL-----SLD--TCGEASV--LEI 436  
 Db 296 SLTRLVQALISYQKKFVAHSNIQQLLSIWDGLPGPRKRKIVDKVICIAOVAALFPLYC 355  
 QY 437 LVVNSKIENRHEMLAVEPINELADKMRKFGAVSYINVSYLCAVTFLTATAYQPLEG 496  
 Db 356 LITVCAPIKRTGQLMKAPF-----MKFLHASLYLFFLILIVS----- 395  
 QY 497 TPYPYRYTVDYRLAG-----EVITLFTGVLFPTVNIKDLF 533  
 Db 396 -----QPADDFVRIFGTRMKKELABQELRQGGTSPSKELIIVWVYIGVWEVEQEIF 450  
 QY 534 MKKCPGVNSL-----FIDFSFOLLFYISYLVLSAALYLAGIE-----ATLAVVVF 580  
 Db 451 ---AVGKMSYLRNMNFIIDPLNSLY--VSVMCLAPAYIQOATEIARDPQMAVTPREKV 505

QY 581 -----ALVLGWMNALYFTRGKLTGTYSI-----MIQKLEPK--DLRFLLVYLPMI 626  
 Db 506 HDPFDQILAEGLFAAANVPSALKLVHLSINPLHGLQSLGRMVIDYKFFITIVLF 565  
 QY 627 GYASALVSLINLNCAMKVCNEDQNTCTVPTP-----SCRDETFSTFLDLFK 675  
 Db 566 AFACGLNQLIMYFAL-----EKSRCYV--LPGCADWGSBGSCMKRRFG-----NLPE 614  
 QY 676 LT-----IGMGDEMLSTKYPVVF--IILVTVIILFTVLLNMLLMGEITVQ 724  
 Db 615 SSQSLFMSFGKVGDDFELSGIKSYTRFWGLMFGSYVINIVYLLNMLMNSNIA 674  
 QY 725 VSKESKHIWK 734  
 Db 675 IDEHSDTEWK 684

## RESULT 14

TRPCL protein " human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 04-Sep-1998  
 C:Accession: I38361  
 R:Wes, P.D.; Chevessich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995  
 A:Title: TRPCL, a human homolog of a Drosophila store-operated channel.  
 A:Reference number: I38361; MUID:96003837; PMID:7568191  
 A:Accession: I38361  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-810 <RES>  
 A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787  
 C:Superfamily: TRPCL protein

Query Match 3.6%; Score 138.5; DB 2; Length 810;  
 Best Local Similarity 18.1%; Pred. No. 0.11;  
 Matches 147; Conservative 126; Mismatches 315; Indels 223; Gaps 36;

QY 12 PEVVELPDESGTSGEAFPLPSLANLPEGSDGSLSPAPADSRAGDGRPNLMKF 71  
 Db 3 PG---IPGRABAVGTHPFPSSPGAWLGSQSGS---GPVGAAPPSS----- 42  
 QY 72 QGAFKRGVNPIDLESTLYESSVVPKPAWDSLFDGYTRHSSDNKRMRKKIIEKO 131  
 Db 43 -----PGLPSPMAWMAALYPTSDLSGASSSL----- 70  
 QY 132 POSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLPILTHKK--RLTDEFRFP 188  
 Db 71 PPSPPSSSSPNEWALK-----DVREYKENTINLKL--FLAACDKGYMVKLILEN 121  
 QY 189 SFGK---TCLP-----KALNLSNGRNDITPVLLD-----IARTGNMEFINSPRDIY 235  
 Db 122 SSQDLININVDVGRNAVITINENDLILQLLDDGCKLMERIQNP---YSTMDV- 177  
 QY 236 YRGQTAHIAIERCKHYVELLVAGADV--HA-QARGRFQPKDGGYFYFGEPLSL 291  
 Db 178 ---AVIIAAHNNYIITMLLKQVSLPKPFAVCECTLCGAKKKKSLRHSRFLI 233  
 QY 292 AACTGNPHVINYITENPHKKADMRDROSGNTVLHLLVLIAD-----NTRNT 339  
 Db 234 YRCLASPALIMTEED-----ILRAPELSADIKELSLVEVERNDYEEL 278  
 QY 340 KFTYKVDLLILKCALFPDSNLEAVLND-----GLSPLMAAATGKI 383  
 Db 279 ARQCKAFADILAQAR--NSRELEVLINHTSDEPLDKGLBERNLSLKLAIYN-- 334  
 QY 384 GIFQHTIREVTDDETRHLSRKFKDMAYGVPVSYLDLSLDTGCEBASVLELLIVNSKI 443  
 Db 335 -----QREFFVQSN---CQGFANTVW---FGOMSGYRRKPKCKKIMVLVIGIF---- 377  
 QY 444 ENRHMLAVPEINELLRDKRRKGAV-----SFYINVSYLCAMITFL--TAYQPLEG 496

Db 378 -----WPLSLCYLIAKX-SQFGRILHTPPMKFIIHGASFTFLLLNLSLVNEDK 430  
 QY 497 TPPEYRTVTVYLRLAGAVITLFTSVLPFTNKKLFMKKCPGANSFLDGSFOLLYFY 556  
 Db 431 NIMGALRIDL-----LILMITGMI--WSDIKLWNE--GLDD-FLBSBRNLSFWM 479  
 QY 557 SVLVIVSAALYIAG-----IAYLAVMY-----PALVIGWMNALYFTRGKL 598  
 Db 480 NSLYLATFALKVVAANKKHFADRKMDAFHPTLVABGLFAFANVLSYLRFFEMVTSI 539  
 QY 599 TGTYSIMIQKILFQDLFRFLVYLLFMIGYASALVSLNPGCANMKVCNEDQNTCTVPTP 658  
 Db 540 LGPLQISGQML-QDPGKFLGFLVLFSTIGLQLDKGYTSK---EQKDC-VGIFC 593  
 QY 659 SCRDETFSTFLDLFKLTIGMGDEMLSTKYPVVF-----IILVTVI 703  
 Db 594 EQGSDNTHSFICGFAL-----FWYIFSLAHVALFVTRFSGBELQSGVAGVIVGTN 647  
 QY 704 IITFVLLNMLIALMGFTVGVSKESKHIWK 734  
 Db 648 VVVIVITKTLVAMLHKSFOLIANHEDKWK 678

## RESULT 15

T00894  
 hypothetical protein F21B7.8 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con-  
 eologis, A.; Ecker, J.R.  
 Submitted to the EMBL Data Library, January 1998  
 A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.  
 A:Reference number: Z14208  
 A:Accession: T00894  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-616 <SHL>  
 A:Cross-references: UNIPROT:Q9LR59; EMBL:AC002560; NID:g2618677; PID:g2809239; GSPDB:GNO  
 C:Genetics:  
 A:Gene: ATSP:F21B7.8  
 A:Map position: 1  
 A:introns: 229/1; 411/3

Query Match 3.6%; Score 137; DB 2; Length 616;  
 Best Local Similarity 20.2%; Pred. No. 0.097;  
 Matches 123; Conservative 93; Mismatches 212; Indels 180; Gaps 30;

QY 161 GSTADLDGLPILTHKKRLTDEFRPESTGTCUPKA--LNLNSGRNDITPVLLDIE 218  
 Db 17 GSISDPDQWTF---KXKDESEIMNPPI--LCAVRAGDKVSLKRIKNDVAKVTRLVD 69  
 QY 219 RTGN-----KREFTNSPP--RDIYRGQTAHIAIERCKHYVELLV--- 258  
 Db 70 NQGNSTLHIAALGHVHVFIIISTFPNLQVNMIGETTLVAAAGSINIYEILVRF 129  
 QY 259 -----AQCAD--VHAQARG-----FQPKDEGGYF----- 283  
 Db 130 TESSSYDAFIARKSKNGDPTALHAALGKHEVAFCILSVXHDVSPKKNDEASPLVAYE 189  
 QY 284 ---FGEPLSLAACMNOPIVNYLLE---NPHKKADM-----ROD 321  
 Db 190 AGYHELVLKMLSSSSPSILASVFSKSVTHAAMKANRDILGIVLRQDPGLIELRNEG 249  
 QY 322 NYVLHALVALADTRENTEKVTVMYDILLKCARLPDSNLEAVLNNDGISPLMAAKTG 381  
 Db 250 RTCLS--YGASMGVCYGIYITIAEPD---KAA-----SSLGVADDGFTPHMAKGG 298  
 QY 382 KIGIFQHTIR---REVTDETRH-----LSRKFKDMAY-----GPVSYSLVLS-- 423  
 Db 299 HVATIKFELKCPDSRELLNNOCONFHVAAIAGSKSVKYLLIKLDEGRKMNNEODINGN 358  
 QY 424 ---LDTGCEASVLELVVNSKIENR---HMLAVEPEINELLRDKRRKGAVSFYINNV 476



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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:07:50 ; Search time 201 Seconds  
(without alignments)  
2124.020 Million cell updates/sec

Title: US-10-090-215-12  
Perfect score: 3858  
Sequence: 1 MADSEGPAPGAEVALLPG.....GVSKSKHMKLQSGRRRL 742

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02: \*  
1: uniprot\_prot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3829	99.2	853	2	Q86YZ6
2	3829	99.2	871	2	Q8NDY7
3	3829	99.2	871	2	Q9HBCO
4	3829	99.2	871	2	Q9GQ92
5	3828	99.2	871	2	Q9HBA0
6	3695	95.8	871	2	Q9BPK8
7	3693	95.7	871	2	Q9BRZ8
8	3689	95.6	871	2	Q9EST6
9	3681	95.4	871	2	Q9EQZ4
10	3636	94.2	873	2	Q9BRZ7
11	3472	90.0	803	2	Q9BRZ7
12	3466	89.8	811	2	Q8NG64
13	3389	87.8	803	2	Q91XR5
14	3284	85.1	852	2	Q9DF53
15	1604.5	41.6	843	2	Q9QFN9
16	1603	41.6	839	2	Q8R5A3
17	1603	41.6	839	2	Q8R5A3
18	1598.5	41.4	839	2	AA513460
19	1580.5	41.0	838	2	Q8K1W1
20	1580	41.0	839	2	Q9UM57
21	1580	41.0	839	2	Q704Y3
22	1580	41.0	839	2	CAFO5661
23	1579.5	40.9	838	2	BAD20301
24	1579.5	40.4	839	2	Q8NBR1
25	1557.5	40.3	839	2	Q9N074
26	1555.5	40.3	839	2	Q9N122
27	1552.5	40.2	842	2	Q6RX08
28	1552.5	40.2	842	2	AA34458
29	1551.5	40.2	839	2	Q9H0G9
30	1551.5	40.2	839	2	Q9H304
31	1369	35.5	778	2	Q9JMS6

32	1324	34.3	761	2	Q9WUD2
33	1332	34.3	761	2	Q9QYH8
34	1332	34.3	762	2	Q9JMT8
35	1331	34.2	791	2	Q8K424
36	1316	34.1	790	2	Q8NFB2
37	1312	34.0	790	2	Q8NDW7
38	1309	33.9	765	2	Q8NBT9
39	1309	33.9	791	2	Q8NBT8
40	1304.5	33.8	756	2	Q6JGX2
41	1304.5	33.8	756	2	Q9WTR1
42	1304.5	33.8	756	2	Q9K7L1
43	1304.5	33.8	756	2	AA66752
44	1298.5	33.7	764	2	Q9Y5S1
45	1287	33.4	764	2	Q9Y670

## ALIGNMENTS

## RESULT 1

Q86YZ6 PRELIMINARY; PRT; 853 AA.

AC Q86YZ6; 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Hypothetical protein TRPV-SV.  
GN Name=TRPV-SV,  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Suzuki S.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN [2]  
RP SEQUENCE FROM N.A.  
RA Suzuki M.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB100308; BAC5864.1; -.  
DR GO; GO:0016021; C:Integral to membrane; IEA.  
DR GO; GO:0005261; P:cation channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR008916; Cat\_channel\_Tryp.  
DR InterPro; IPR008996; CytoK\_III\_Like.  
DR InterPro; IPR005821; Ion\_chan.  
DR InterPro; IPR004729; TRPChannel.  
DR InterPro; IPR008347; Vanil\_receptor.  
DR InterPro; IPR008348; Vanil\_receptor2.  
DR Pfam; PF00023; ANK\_3.  
DR Pfam; PF00520; Ion\_trans\_1.  
DR PRINTS; PRO1415; ANKYRIN.  
DR PRINTS; PRO1768; TRPReceptor.  
DR PRINTS; PRO1769; VRL2RECEPTOR.  
DR SMART; SMO0248; ANK\_3.  
DR TIGRfams; TIGR00870; trp\_1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR ANK repeat; Hypothetical protein; Ion transport; Ionic channel;  
KW Transmembrane; Transport.  
SQ SEQUENCE 853 AA; 96448 MW; EAA07196606AED20 CMC64;

Query Match 99.2%; Score 3829; DB 2; Length 853;  
Best local Similarity 100.0%; Pred. No. 4e-233;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSEGPAPGAEVALLPGDESGTPGGEAPPLSLANLTFPGEDGSLSPSPADSRPAPG 60  
Db 1 MADSEGPAPGAEVALLPGDESGTPGGEAPPLSLANLTFPGEDGSLSPSPADSRPAPG 60  
Qy 61 GDGRPNLMKRFQGAERKGVNPNPDLLESTLYESSVVPKPKAPMDSLFDYGYVRRHSSDN 120

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Db      |||||
61  GDGRNLMKFGAGRKGVNPIDLLSESTLYSSVVPCKAPMDSLFYGYRRHSSDN 120
Qy      121 KMRKKIIEKQSPKAPAPPPPIIKVNNRPIIDIVSRGSTADLDGLPLTHKKRL 180
Db      121 KMRKKIIEKQSPKAPAPPPPIIKVNNRPIIDIVSRGSTADLDGLPLTHKKRL 180
Qy      181 TDEEPREPTGKTCIPKALINLSNGRNDITPVLLDIAERTGNMREINSPPFDIYYRGQT 240
Db      181 TDEEPREPTGKTCIPKALINLSNGRNDITPVLLDIAERTGNMREINSPPFDIYYRGQT 240
Qy      241 ALHAIERRCKHYVELLVAGADVAHQAGRRFPQPDGEGYFYFGELPLSLAQTNPPI 300
Db      241 ALHAIERRCKHYVELLVAGADVAHQAGRRFPQPDGEGYFYFGELPLSLAQTNPPI 300
Qy      301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
Db      301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
Qy      361 NLEAVLNDGLSPLMMAAKTGKIGIFOHIIIRREVTDDETRHLSRKFKDMAVGPVYSSLYD 420
Db      361 NLEAVLNDGLSPLMMAAKTGKIGIFOHIIIRREVTDDETRHLSRKFKDMAVGPVYSSLYD 420
Qy      421 LSSLDTCGEASVLEILVYNSKIENHMLAVEPINELDRKRRKGAVSFYINVSYLIC 480
Db      421 LSSLDTCGEASVLEILVYNSKIENHMLAVEPINELDRKRRKGAVSFYINVSYLIC 480
Qy      481 ANVIFLTAYYQPLRGTPPYRRTTYDYRLAGEVITLFTGVLPFTNKKDLPMKKCPGV 540
Db      481 ANVIFLTAYYQPLRGTPPYRRTTYDYRLAGEVITLFTGVLPFTNKKDLPMKKCPGV 540
Qy      541 NSLFDIGSFQLLYFISVLYVSAALYLAGIEAVLAWVFAVLGMNNAIYFRGLKLTG 600
Db      541 NSLFDIGSFQLLYFISVLYVSAALYLAGIEAVLAWVFAVLGMNNAIYFRGLKLTG 600
Qy      601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNBDQNCVPTPSC 660
Db      601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNBDQNCVPTPSC 660
Qy      661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTVYIILTFVLLNMLIAME 720
Db      661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTVYIILTFVLLNMLIAME 720
Qy      721 TVGQVSKESKHWKLTQ 736
Db      721 TVGQVSKESKHWKLTQ 736

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DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006812; P:cation transport; IEA.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR002111; Cat channel TrpL.
DR      InterPro; IPR008996; CytoC IL1 like.
DR      InterPro; IPR005821; Ion trans-
DR      InterPro; IPR004729; TRP channel.
DR      InterPro; IPR008347; Vanil_1 receptor.
DR      InterPro; IPR008348; Vanil_2 receptor.
DR      Pfam; PF00023; Ank; 3.
DR      Pfam; PF00520; Ion trans; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      PRINTS; PR01769; VRL2RECEPTOR.
DR      SMART; SM00248; ANK; 3.
DR      TIGRFAMs; TIGR00870; trp; 1.
DR      PROSITE; PS50088; ANK REPEAT; 1.
DR      PROSITE; PS50297; ANK REP REGION; 1.
KW      ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW      Transport.
SQ      SEQUENCE 871 AA; 98280 MW; C62056B86C5A6FB6 CRC64;

Query Match      99.2%; Score 3829; DB 2; Length 871;
Best Local Similarity 100.0%; Pred. No. 4.1e-233;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  MADSSRGPRAGGEVAELPDGSGTPGGEAFPLSLANLFEGEDGSLSPSPADASRPAP 60
1  MADSSRGPRAGGEVAELPDGSGTPGGEAFPLSLANLFEGEDGSLSPSPADASRPAP 60
61  GDGRNLMKFGAGRKGVNPIDLLSESTLYSSVVPCKAPMDSLFYGYRRHSSDN 120
61  GDGRNLMKFGAGRKGVNPIDLLSESTLYSSVVPCKAPMDSLFYGYRRHSSDN 120
121 KMRKKIIEKQSPKAPAPPPPIIKVNNRPIIDIVSRGSTADLDGLPLTHKKRL 180
121 KMRKKIIEKQSPKAPAPPPPIIKVNNRPIIDIVSRGSTADLDGLPLTHKKRL 180
181 TDEEPREPTGKTCIPKALINLSNGRNDITPVLLDIAERTGNMREINSPPFDIYYRGQT 240
181 TDEEPREPTGKTCIPKALINLSNGRNDITPVLLDIAERTGNMREINSPPFDIYYRGQT 240
241 ALHAIERRCKHYVELLVAGADVAHQAGRRFPQPDGEGYFYFGELPLSLAQTNPPI 300
241 ALHAIERRCKHYVELLVAGADVAHQAGRRFPQPDGEGYFYFGELPLSLAQTNPPI 300
301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRNTKFTVTKMYDILLKCARLPDS 360
361 NLEAVLNDGLSPLMMAAKTGKIGIFOHIIIRREVTDDETRHLSRKFKDMAVGPVYSSLYD 420
361 NLEAVLNDGLSPLMMAAKTGKIGIFOHIIIRREVTDDETRHLSRKFKDMAVGPVYSSLYD 420
421 LSSLDTCGEASVLEILVYNSKIENHMLAVEPINELDRKRRKGAVSFYINVSYLIC 480
421 LSSLDTCGEASVLEILVYNSKIENHMLAVEPINELDRKRRKGAVSFYINVSYLIC 480
481 ANVIFLTAYYQPLRGTPPYRRTTYDYRLAGEVITLFTGVLPFTNKKDLPMKKCPGV 540
481 ANVIFLTAYYQPLRGTPPYRRTTYDYRLAGEVITLFTGVLPFTNKKDLPMKKCPGV 540
541 NSLFDIGSFQLLYFISVLYVSAALYLAGIEAVLAWVFAVLGMNNAIYFRGLKLTG 600
541 NSLFDIGSFQLLYFISVLYVSAALYLAGIEAVLAWVFAVLGMNNAIYFRGLKLTG 600
601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNBDQNCVPTPSC 660
601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNPKANMKVCNBDQNCVPTPSC 660
661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTVYIILTFVLLNMLIAME 720
661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIILVTVYIILTFVLLNMLIAME 720

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QY 721 TWGVSKSKHIMKIQ 736
DB 721 TWGVSKSKHIMKIQ 736

RESULT 3
Q9HBCO PRELIMINARY; PRT; 871 AA.
AC Q9HBCO;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE OTRPC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=renal cortex;
RX MEDLINE=20482174; PubMed=11025659;
RA Strickman R., Harteneck C., Numenmacher K., Schultz G., Plant T.D.;
RT "OTRPC4, a nonselective cation channel that confers sensitivity to
RT extracellular osmolarity";
RU Nat. Cell Biol. 2:695-702(2000).
DR EMBL; AF258465; AAG16127.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0015281; F:nonselective cation channel activity; NAS.
DR GO; GO:0006816; P:calcium ion transport; NAS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripI.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1768; TRPRECEPTOR.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; ttp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 871 AA; 98294 MW; C62056B86DEA6FB6 CRC64;

Query Match 99.2%; Score 3829; DB 2; Length 871;
Beet Local Similarity 100.0%; Pred. No. 4,1e-233;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAPGGEVAELPGDESGTGGGEAPPLSSIANLFGEGGSLSPSPADSRPAGP 60
DB 1 MADSSGPRAPGGEVAELPGDESGTGGGEAPPLSSIANLFGEGGSLSPSPADSRPAGP 60
QY 61 GDGSPNLRMKFQAGFRKGVNPIDLLSTLYESSVVPKPKAPMDLSLFDYTYRHSSDN 120
DB 61 GDGSPNLRMKFQAGFRKGVNPIDLLSTLYESSVVPKPKAPMDLSLFDYTYRHSSDN 120
QY 121 KRWKKTIEKOPQSPKAPAPPPILKYFNPPIIFDIYVSRGSTDLDGLPFLTHKKRL 180
DB 121 KRWKKTIEKOPQSPKAPAPPPILKYFNPPIIFDIYVSRGSTDLDGLPFLTHKKRL 180
QY 181 TDEFRPSTGKTCLPALANLNSGRNDTIPVLLDIERTGNMSEFINSPPRDIYYGQT 240
DB 181 TDEFRPSTGKTCLPALANLNSGRNDTIPVLLDIERTGNMSEFINSPPRDIYYGQT 240
QY 241 ALHAIERRCKHYVELLVAQADVHAQARGFPOPKDEGFGYFGEGLPLSLAAGTNPPI 300
DB 241 ALHAIERRCKHYVELLVAQADVHAQARGFPOPKDEGFGYFGEGLPLSLAAGTNPPI 300

```

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QY 301 VNYLTENPKKADMERODSRGNTVLAVALADNTRENTKFTYKAYDILLKCARLPSPS 360
DB 301 VNYLTENPKKADMERODSRGNTVLAVALADNTRENTKFTYKAYDILLKCARLPSPS 360
QY 361 NLEAVLNNDGLSPIMAAKTKIGIPQHIIIRREVTDETRHLSRKKDWAAGVPVSYLD 420
DB 361 NLEAVLNNDGLSPIMAAKTKIGIPQHIIIRREVTDETRHLSRKKDWAAGVPVSYLD 420
QY 421 LSLDTGGEASVLEILVNSKIENRHEMLAEPINELRDQWRKGAVSFYINVSILC 480
DB 421 LSLDTGGEASVLEILVNSKIENRHEMLAEPINELRDQWRKGAVSFYINVSILC 480
QY 481 AMVIFTLAAVYQPLEGTPPYPRITVDYKRLAGEVITLFTGYLFPFTIKDLPKKCPGV 540
DB 481 AMVIFTLAAVYQPLEGTPPYPRITVDYKRLAGEVITLFTGYLFPFTIKDLPKKCPGV 540
QY 541 NSLFTDGSFQILYFYISVLYVSALVYAGIAYLAVVFAVLGMNNAVYTRGKILTG 600
DB 541 NSLFTDGSFQILYFYISVLYVSALVYAGIAYLAVVFAVLGMNNAVYTRGKILTG 600
QY 601 TYSIMIOKILFPDLFRFLLVYLFMIGYASALVSLNPGANKKCNEDQNTCTVPTPSC 660
DB 601 TYSIMIOKILFPDLFRFLLVYLFMIGYASALVSLNPGANKKCNEDQNTCTVPTPSC 660
QY 661 RDSFTSTFLDLFLITGMGDIEMLSSTKYVVFIIILVYIIILFVLLNMLALMGE 720
DB 661 RDSFTSTFLDLFLITGMGDIEMLSSTKYVVFIIILVYIIILFVLLNMLALMGE 720
QY 721 TWGVSKSKHIMKIQ 736
DB 721 TWGVSKSKHIMKIQ 736

RESULT 4
Q96G92 PRELIMINARY; PRT; 871 AA.
ID Q96G92;
AC Q96G92;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Vanilloid receptor like channel-2.
GN Name=VRL-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032427; BAB69040.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripI.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1768; TRPRECEPTOR.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; ttp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
Transport.

```

SQ SEQUENCE 871 AA; 98266 MW; C62056A401ECA8B6 CRC64;  
 Query Match 99.2%; Score 3829; DB 2; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-23;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAELPGDESGTGGGAFFPLSLANLFEGBDGLSPSPDASRPAGP 60  
 DB 1 MADSSRGPRAGGEVAELPGDESGTGGGAFFPLSLANLFEGBDGLSPSPDASRPAGP 60  
 QY 61 GGGPRLRMKFOGAFKGVNPIDILESTLYSSVVGPKKAPMDSLFDYGYRRHSSDN 120  
 DB 61 GGGPRLRMKFOGAFKGVNPIDILESTLYSSVVGPKKAPMDSLFDYGYRRHSSDN 120  
 QY 121 KWRKKIIEKOPSPAPAPPPILKYNNRPLDIYRSSTADLDGLPLTHKKRL 180  
 DB 121 KWRKKIIEKOPSPAPAPPPILKYNNRPLDIYRSSTADLDGLPLTHKKRL 180  
 QY 181 TDEFRPESTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240  
 DB 181 TDEFRPESTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240  
 QY 241 ALHIAIERCKHYVELVAQADVHAQARGFFQPDGEGYFFGELPLSLAATNOPIH 300  
 DB 241 ALHIAIERCKHYVELVAQADVHAQARGFFQPDGEGYFFGELPLSLAATNOPIH 300  
 QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTYKMYDILLKCARLPDS 360  
 DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTYKMYDILLKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPDMAAKTGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420  
 DB 361 NLEAVLNNDGLSPDMAAKTGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420  
 QY 421 LSSLDTCGEASVLEILVYNSKIENHHEMLAVEPINELLDKRRKGAVSFYINVSYL 480  
 DB 421 LSSLDTCGEASVLEILVYNSKIENHHEMLAVEPINELLDKRRKGAVSFYINVSYL 480  
 QY 481 AMVIFTLTAYYOPLEGPPYPRRTYDYLRLAGEVITLFTGVLPFTNIDLFMKKCPGV 540  
 DB 481 AMVIFTLTAYYOPLEGPPYPRRTYDYLRLAGEVITLFTGVLPFTNIDLFMKKCPGV 540  
 QY 541 NSLFLDGSFQLYFYISVLYVSALYLAGIEAYLAVMVFALVGMNNAFYTRGLKLTG 600  
 DB 541 NSLFLDGSFQLYFYISVLYVSALYLAGIEAYLAVMVFALVGMNNAFYTRGLKLTG 600  
 QY 601 TYSIMTQKILFKDLFRPLVYLLFMIGYASALVSLNPGANMKVCNEDOTNCTVPTPSC 660  
 DB 601 TYSIMTQKILFKDLFRPLVYLLFMIGYASALVSLNPGANMKVCNEDOTNCTVPTPSC 660  
 QY 661 RDETFSTFLDLFKLTIKGDLEMLSTXYPVVFIIILVYIILTFVLLNMLALMGE 720  
 DB 661 RDETFSTFLDLFKLTIKGDLEMLSTXYPVVFIIILVYIILTFVLLNMLALMGE 720  
 QY 721 TVGQVSKESKHVWLQ 736  
 DB 721 TVGQVSKESKHVWLQ 736

RESULT 5  
 Q9HBA0 PRELIMINARY; PRT; 871 AA.  
 AC Q9HBA0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Vanilloid receptor-related osmotically activated channel.  
 OS Name=VROAC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20531888; PubMed=11081638;  
 RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,  
 RA Sali A., Hudepeth A.J., Friedman J.M., Heller S.;  
 RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a  
 RT candidate vertebrate osmoreceptor.";  
 RL Cell 103:525-535(2000).  
 DR EMBL; AF263523; AAG28029.1; -;  
 DR GO; GO:0016021; C:Integral to membrane; IEA.  
 DR GO; GO:0005261; F:cation channel activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_Trlp.  
 DR InterPro; IPR008996; CytoK\_IL1\_like.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR01768; TRPVRECEPTOR.  
 DR PRINTS; PR01769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRfam6; TIGR00670; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_RBP\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.

SQ SEQUENCE 871 AA; 98265 MW; A86FB6C9103C19 CRC64;  
 Query Match 99.2%; Score 3828; DB 2; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 4.7e-23;  
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSRGPRAGGEVAELPGDESGTGGGAFFPLSLANLFEGBDGLSPSPDASRPAGP 60  
 DB 1 MADSSRGPRAGGEVAELPGDESGTGGGAFFPLSLANLFEGBDGLSPSPDASRPAGP 60  
 QY 61 GGGPRLRMKFOGAFKGVNPIDILESTLYSSVVGPKKAPMDSLFDYGYRRHSSDN 120  
 DB 61 GGGPRLRMKFOGAFKGVNPIDILESTLYSSVVGPKKAPMDSLFDYGYRRHSSDN 120  
 QY 121 KWRKKIIEKOPSPAPAPPPILKYNNRPLDIYRSSTADLDGLPLTHKKRL 180  
 DB 121 KWRKKIIEKOPSPAPAPPPILKYNNRPLDIYRSSTADLDGLPLTHKKRL 180  
 QY 181 TDEFRPESTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240  
 DB 181 TDEFRPESTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRGQT 240  
 QY 241 ALHIAIERCKHYVELVAQADVHAQARGFFQPDGEGYFFGELPLSLAATNOPIH 300  
 DB 241 ALHIAIERCKHYVELVAQADVHAQARGFFQPDGEGYFFGELPLSLAATNOPIH 300  
 QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTYKMYDILLKCARLPDS 360  
 DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTEENTKFTYKMYDILLKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPDMAAKTGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420  
 DB 361 NLEAVLNNDGLSPDMAAKTGKIGIFOHIIIRREVTDERTHLSRKFDMAVGPVSSLYD 420  
 QY 421 LSSLDTCGEASVLEILVYNSKIENHHEMLAVEPINELLDKRRKGAVSFYINVSYL 480  
 DB 421 LSSLDTCGEASVLEILVYNSKIENHHEMLAVEPINELLDKRRKGAVSFYINVSYL 480  
 QY 481 AMVIFTLTAYYOPLEGPPYPRRTYDYLRLAGEVITLFTGVLPFTNIDLFMKKCPGV 540  
 DB 481 AMVIFTLTAYYOPLEGPPYPRRTYDYLRLAGEVITLFTGVLPFTNIDLFMKKCPGV 540  
 QY 541 NSLFLDGSFQLYFYISVLYVSALYLAGIEAYLAVMVFALVGMNNAFYTRGLKLTG 600

Dd		541 NSLFFIDSGQLTFYFISVAVIYSALYAGIEAYLVAMVFALVGMMNALFYRGLKLTG	600
Qy		601 TYSIMQKLIFNDLEPFLIVYLTFMIGSALSLSLANPCANMYCNEDQNTCTVPYPSPC	660
Dd		601 TYSIMQKLIFNDLEPFLIVYLTFMIGSALSLSLANPCANMKVCNEDQNTCTVPYPSPC	660
Qy		661 RSEFTSTFLDLFKTLTIGMDLEMISTCYTPVVFIIILVTYIIILFPVLIINLIALMG	720
Dd		661 RSEFTSTFLDLFKTLTIGMDLEMISTCTIPVVFIIILVTYIIILFPVLIINLIALMG	720
Qy	721 TVGVSKESKHIMKIQ	736	
Dd	721 TVGVSKESKHIMKIQ	736	
<hr/>			
RESULT 6			
Q9EPK8	PRELIMINARY;	PRT; 871 AA.	
ID Q9EPK8;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
GN Name=Trpv4; Synonyms=Trpl2;			
OS Mus musculus (Mouse).			
OC Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxId=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Kidney;			
RX MEDLINE=2054752; PubMed=11094154;			
RA Wisenbach U., Boedding M., Freichel M., Flockerzi V.,			
RT "Trpl2, a novel Trp related protein from kidney.";			
RL FEBS Lett. 485:127-134(2000) .			
DR EMBL, AJ296078: CAC20703.1. -			
DR MGD, MGI:1926845: Trpv4.			
DR GO, GO:0005262; F:calcium channel activity; IDA.			
DR GO, GO:0005034; P:osmosensor activity; IDA.			
DR GO, GO:0042538; P:hypertonic salinity response; IMP.			
DR GO, GO:0007231; P:osmosensory signaling pathway; IDA.			
DR GO, GO:0047484; P:regulation of response to osmotic stress; IMP.			
DR GO, GO:003103; P:vasopressin secretion; IMP.			
DR InterPro; IPR002110; ANK.			
DR InterPro; IPR002111; Cat_channel_TrpL.			
DR InterPro; IPR008996; CytoK_IL1_like.			
DR InterPro; IPR005821; Ion trans.			
DR InterPro; IPR004729; TRPChannel.			
DR InterPro; IPR008347; Vanil_receptor.			
DR InterPro; IPR008348; Vanil_receptor2.			
DR Pfam; PF00023; Ank; 3.			
DR Pfam; PF00520; Ion trans; 1.			
DR PRINTS; PRO1768; TRPRECEPTOR.			
DR PRINTS; PRO1769; VRL2RECEPTOR.			
DR SMART; SM00248; ANK; 3.			
DR TIGRFAMS; TIGR00670; trp; 1.			
DR PROSITE; PS50088; ANK_REPEAT; 1.			
DR PROSITE; PS50297; ANK REP REGION; 1.			
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;			
KW Transport.			
SO SEQUENCE	871 AA;	98026 MW;	5BAC6E33FB9CEA05 CRC64;
<hr/>			
Query Match 95.8%; Score 3695; DB 2; Length 871;			
Best Local Similarity 95.7%; Pred. No.1,2e-224;			
Matches 704; Conservative 16; Mismatches 16; Indels 0; Gaps 0;			
Qy	1 MADSSGGRRAPGGEVALIPIGDSGTGGGAEPPLSLANTLFEGDSDLSPPADASRPAPGP	60	
Dd	1 MADGGDGRRAPGGEVAEPPEGDSGTGGGAEPPLSLANTLFEGEGSSSLSPVASRPAPGP	60	
Oy	61 GDGPNLRMRKGAFPRKGVNPRIILLSESTLYESSVYGPGRKAPADSLLFDYGYTRHSSDN	120	

Db	61	GGGRPLRKPGAGFRKGVPNPDLLESTLYESSVVGPKKAMDSLFDYGYRRHSDN	120
QY	121	KEMRKIIIEKOPSPKAPAPPEPPIIKVENRPILFDIVSRGSTADLDGLPILTHKKRL	180
Db	121	KEMRRKVEKOPSPKAPAPPEPPIIKVENRPILFDIVSRGSTADLDGLPILTHKKRL	180
QY	181	TDEPREPESTGTCCLPKALLNSGNDPTLPVLDIAERTGNMREPIINSFROIYYRGQT	240
Db	181	TDEPREPESTGTCCLPKALLNSGNDPTLPVLDIAERTGNMREPIINSFROIYYRGQT	240
QY	241	ALHIIIERCKHYVELLVAAQGDVHAQAAGRFPOPEDEGYPFGGLPLSLACTOPHI	300
Db	241	SLHIIIERCKHYVELLVAAQGDVHAQAAGRFPOPEDEGYPFGGLPLSLACTOPHI	300
QY	301	VNYLTENPHKADMRRODSRGNTVLAVALADNTRERNTKFTYKMDLLILCKARLPDS	360
Db	301	VNYLTENPHKADMRRODSRGNTVLAVALADNTRERNTKFTYKMDLLILCKARLPDS	360
QY	361	NIEAVLANDGSLPLMMAAKTGKIGLFOHIIIRREVTDEDTRLSRKFKDWAAGVYSSLYD	420
Db	361	NIEAVLANDGSLPLMMAAKTGKIGLFOHIIIRREVTDEDTRLSRKFKDWAAGVYSSLYD	420
QY	421	LSLSDTCGEESVLELIVYNSKIENRHEMLAREPINELLDKWRKGAVSFYINVSYLK	480
Db	421	LSLSDTCGEESVLELIVYNSKIENRHEMLAREPINELLDKWRKGAVSFYINVSYLK	480
QY	481	AMVIFTLTAAVYQPLEGTEPPYPRYTVDYRLALAGEVITLFTGYLFPFTNKKDLPMKKCPGV	540
Db	481	AMVIFTLTAAVYQPLEGTEPPYPRYTVDYRLALAGEVITLFTGYLFPFTNKKDLPMKKCPGV	540
QY	541	NSLFTDGGSPOLIYFYIVLVISAALYLAGIAYLAVWFAVLGWMNALYFTRGKLKG	600
Db	541	NSLFTDGGSPOLIYFYIVLVISAALYLAGIAYLAVWFAVLGWMNALYFTRGKLKG	600
QY	601	TYSIMIQILFPROLFRFLIVYLITLPMIGASALVSLNPGCANMKVCNEDOTNCTVPTYBSC	660
Db	601	TYSIMIQILFPROLFRFLIVYLITLPMIGASALVSLNPGCANMKVCNEDOTNCTVPTYBSC	660
QY	661	RDSEFTSFFLDLFLUTLTGMDLEMLSTKRPVVFIIILVTYIILTFVYLLNMLTALMGE	720
Db	661	RDSEFTSFFLDLFLUTLTGMDLEMLSTKRPVVFIIILVTYIILTFVYLLNMLTALMGE	720
QY	721	TVGVYSKESKHIWKIQ 736	
Db	721	TVGVYSKESKHIWKIQ 736	
RESULT 7			
Q9ERZ8		PRELIMINARY; PRT; 871 AA.	
ID	Q9ERZ8		
AC	Q9ERZ8		
DT	01-MAR-2001 (Tremblrel. 16, Created)		
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	Vanilloid receptor-related osmotically activated channel.		
GN	Name=Vroac;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RX	MEDLINE=20531888; PubMed=11081638;		
RA	Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,		
RA	Sali A., Hudepeth A.J., Friedman J.M., Heller S.;		
RT	"Vanilloid receptor-related osmotically activated channel (VR-OAC), a		
RT	candidate vertebrate osmoreceptor.";		
RL	Cell 103:525-535(2000).		
DR	EMBL: AF263521; AAC08027.1; -		
DR	GO: GO:0016021; C:Integral to membrane; IEA.		
DR	GO: GO:0005261; F:cation channel activity; IEA.		
DR	GO: GO:0004872; F:receptor activity; IEA.		

DR GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_TripL.  
 DR InterPro; IPR008986; CytoK\_IL1\_Like.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PR01768; TRP\_RECEPTOR.  
 DR PRINTS; PR01769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trip; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.  
 KM ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.  
 SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 95.7%; Score 3693; DB 2; Length 871;

Best Local Similarity 95.5%; Pred. No. 1.6e-224;  
 Matches 703; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 MADSSRGPRAPGEVAELPGDESGTPGGEAPPLSLANLFEGBDGLSPSPADASRPAGP 60  
 DB 1 MADPGGPRAPAGDVAEPGDESGTSGGAPFLSLANLFEGBDGLSPSPADASRPAGP 60  
 QY 61 GNGRPILRMKFGQARRKGVNPIDILESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120  
 DB 61 GNGRPILRMKFGQARRKGVNPIDILESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120  
 QY 121 KMRKKIIEKOPSPKAPAPPPILKVFNRPIIFDIVSRGSTADLDGLPILLTHKKRL 180  
 DB 121 KMRKKIIEKOPSPKAPAPPPILKVFNRPIIFDIVSRGSTADLDGLPILLTHKKRL 180  
 QY 181 TDEEPEPSTGKTCPLKALINLSNGNDTTPVLLDIAERTGNMREPIINSPFRDIYRGQT 240  
 DB 181 TDEEPEPSTGKTCPLKALINLSNGNDTTPVLLDIAERTGNMREPIINSPFRDIYRGQT 240  
 QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPOKDEGGYFPGGLPFLSLAQTNPPI 300  
 DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPOKDEGGYFPGGLPFLSLAQTNPPI 300  
 QY 301 VNYLTENPKKADMRQDSRGNTVLAVALADNTRKTEKVTYKATDILLKCARLPDS 360  
 DB 301 VNYLTENPKKADMRQDSRGNTVLAVALADNTRKTEKVTYKATDILLKCARLPDS 360  
 QY 361 NLEAVLNNDGLSPILMAAATGKIGIFQHTIRREVTDEBTRHLSRKCKDMAVGYVSSLYD 420  
 DB 361 NLEAVLNNDGLSPILMAAATGKIGIFQHTIRREVTDEBTRHLSRKCKDMAVGYVSSLYD 420  
 QY 421 LSLDTCGGEASVLELIVNSKIENRHEMLAVEPINELLRDKRKGAVSFYINVSYL 480  
 DB 421 LSLDTCGGEASVLELIVNSKIENRHEMLAVEPINELLRDKRKGAVSFYINVSYL 480  
 QY 481 AMVIFLITAYQPLEGTPPYRYRTVDYLALAGEVITLFTGVLPFTNIRKDLFMKCPGV 540  
 DB 481 AMVIFLITAYQPLEGTPPYRYRTVDYLALAGEVITLFTGVLPFTNIRKDLFMKCPGV 540  
 QY 541 NSLFIIDGSPQLLYFISVLTIVSAALYLAGIEAYLAMVAVLVGMNNAFYTRGLKLTG 600  
 DB 541 NSLFIIDGSPQLLYFISVLTIVSAALYLAGIEAYLAMVAVLVGMNNAFYTRGLKLTG 600  
 QY 601 TYSIMOKILFKDLERFLVYLLFMIGYASALVILNPCAMKVCNEDQNTCTVTPSC 660  
 DB 601 TYSIMOKILFKDLERFLVYLLFMIGYASALVILNPCAMKVCNEDQNTCTVTPSC 660  
 QY 661 ROSESTFLLDLFKLITIGMDLEMLSTKXVVFILLVYIILTFVLLNMLALMGE 720  
 DB 661 ROSESTFLLDLFKLITIGMDLEMLSTKXVVFILLVYIILTFVLLNMLALMGE 720  
 QY 721 TVGVSKEKSHIMKQ 736

DB 721 TVGVSKEKSHIMKQ 736

RESULT 8  
 Q9876 PRELIMINARY; PRT; 871 AA.

AC Q9876; AC  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE OTRPC4 cation channel.  
 GN Name=Trpv4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvEv;  
 RC MEDLINE=20482174; PubMed=11025659;  
 RA Stroetmann R., Hatteneck C., Nimmacher K., Schultz G., Plant T.D.;  
 RT "OTRPC4, a nonselective cation channel that confers sensitivity to  
 extracellular osmolarity.";  
 RL Nat. Cell Biol. 2:695-702(2000).

DR EMBL; AF208026; A017543.1; -.

DR MGD; MGI:1926945; Trpv4.  
 DR GO; GO:0005262; F:calcium channel activity; IDA.

DR GO; GO:0005034; P:osmosensor activity; IDA.

DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.

DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.

DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.

DR GO; GO:0030103; P:vasopressin secretion; IMP.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR002111; Cat\_channel\_TripL.

DR InterPro; IPR008986; CytoK\_IL1\_Like.

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR004729; TRPChannel.

DR InterPro; IPR008347; Vanil\_receptor.

DR InterPro; IPR008348; Vanil\_receptor2.

DR Pfam; PF00023; Ank; 3.

DR Pfam; PF00520; Ion\_trans; 1.

DR PRINTS; PR01768; TRP\_RECEPTOR.

DR PRINTS; PR01769; VRL2RECEPTOR.

DR SMART; SM00248; ANK; 3.

DR TIGRFAMs; TIGR00870; trip; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 1.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

KM ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.

SQ SEQUENCE 871 AA; 98069 MW; 2B228D554083F00A CRC64;

Query Match 95.6%; Score 3689; DB 2; Length 871;

Best Local Similarity 95.5%; Pred. No. 2.8e-224;  
 Matches 703; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MADSSRGPRAPGEVAELPGDESGTPGGEAPPLSLANLFEGBDGLSPSPADASRPAGP 60  
 DB 1 MADPGGPRAPAGDVAEPGDESGTSGGAPFLSLANLFEGBDGLSPSPADASRPAGP 60  
 QY 61 GNGRPILRMKFGQARRKGVNPIDILESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120  
 DB 61 GNGRPILRMKFGQARRKGVNPIDILESTLYESSVVGPKKXPMDSLFYGYTRHSSDN 120  
 QY 121 KMRKKIIEKOPSPKAPAPPPILKVFNRPIIFDIVSRGSTADLDGLPILLTHKKRL 180  
 DB 121 KMRKKIIEKOPSPKAPAPPPILKVFNRPIIFDIVSRGSTADLDGLPILLTHKKRL 180  
 QY 181 TDEEPEPSTGKTCPLKALINLSNGNDTTPVLLDIAERTGNMREPIINSPFRDIYRGQT 240  
 DB 181 TDEEPEPSTGKTCPLKALINLSNGNDTTPVLLDIAERTGNMREPIINSPFRDIYRGQT 240  
 QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPOKDEGGYFPGGLPFLSLAQTNPPI 300  
 DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPOKDEGGYFPGGLPFLSLAQTNPPI 300

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Db 241 SLHIAIERCKHYVELVAQADVHAQARGFPQKDEGYPYFGEPLSLAAGTNOPIH 300
QY 301 VNYLTENPHKKAQDMRQDSRGNTVLAHVAIADNTRENTKPYTKYDILLKCARLPDS 360
Db 301 VNYLTENPHKKAQDMRQDSRGNTVLAHVAIADNTRENTKPYTKYDILLKCARLPDS 360
QY 361 NLEAVLNNDGSLPMMAAATGKIGFOHIIREVTDEBTRHLSRKFQDMAYGPVYSSLYD 420
Db 361 NLEAVLNNDGSLPMMAAATGKIGFOHIIREVTDEBTRHLSRKFQDMAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEIIVYNSKIENHHEMLAVEPINELRDKMRKFGASFTINAVSYIC 480
Db 421 LSSLDTCGEASVLEIIVYNSKIENHHEMLAVEPINELRDKMRKFGASFTINAVSYIC 480
QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNIKDLFMKCGPV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNIKDLFMKCGPV 540
QY 541 NSLFDGSPQLLYFYISVLYVSAALYAGIBAYLAVMVFALVGMNNAIYFTGKLXLTG 600
Db 541 NSLFDGSPQLLYFYISVLYVSAALYAGIBAYLAVMVFALVGMNNAIYFTGKLXLTG 600
QY 601 TYSIMIQILFKDLFRFLVYLFMIGYASALVSLNFCANMKCNEDQNTCTVPTPASC 660
Db 601 TYSIMIQILFKDLFRFLVYLFMIGYASALVSLNFCANMKCNEDQNTCTVPTPASC 660
QY 661 RDSEFTSFLLDLFKLITGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
Db 661 RDSEFTSFLLDLFKLITGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
QY 721 TVGVSKESKHIWKLQ 736
Db 721 TVGVSKESKHIWKLQ 736

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RESULT 9

Q9EQZ4 PRELIMINARY; PRT; 871 AA.

AC Q9EQZ4, 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

Db 01 channel.

GN Name=Trpv4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA MEDLINE=22692536; PubMed=12692122;

RT "Impaired pressure sensation in mice lacking TRPV4.";

RL J. Biol. Chem. 278:22664-22668(2003).

DR EMBL; AB021875; BAAB3731.2; -.

DR MGI; MGI:1926945; Trpv4.

DR GO; GO:0005262; F:calcium channel activity; IDA.

DR GO; GO:0005034; F:osmosensory activity; IDA.

DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.

DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.

DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.

DR GO; GO:0030103; P:vasopressin secretion; IMP.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR002111; Cat channel TrpL.

DR InterPro; IPR008996; Cytok IL1 like.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR004723; TRPChannel.

DR InterPro; IPR008347; Vanil\_receptor.

DR InterPro; IPR008348; Vanil\_receptor2.

DR Pfam; PF00023; Ank; 3.

DR Pfam; PF00520; Ion trans; 1.

DE PRINTS; PR01768; TRPVRECEPTOR.

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DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAM6; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionc channel; Transmembrane; Transport.
SQ SEQUENCE 871 AA; 98060 MW; 3285AE576D32DD95 CRC64;

Query Match          95.4%; Score 3681; DB 2; Length 871;
Best Local Similarity 95.2%; Pred. No. 9e-224;
Matches 701; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 MADSEGPAGGEVAELPGDESGTGGAPPLSLANIFEGEDSLSPSPADARPAQ 60
Db 1 MADPDGGRAPAGVAEPGDESGTGGAPPLSLANIFEGEDSLSPSPADARPAQ 60
QY 61 GDRPNLPMKQGAFAKGVNPIDLESTLYESSVYPGPKAPMDSLFDYGRHSSDN 120
Db 61 GDRPNLPMKQGAFAKGVNPIDLESTLYESSVYPGPKAPMDSLFDYGRHSSDN 120
QY 121 KWRKRIIEKQPOSPKAPAPPPILKFNRPILFDYVRSSTADLDGLPLTHKKRL 180
Db 121 KWRKRIIEKQPOSPKAPAPPPILKFNRPILFDYVRSSTADLDGLPLTHKKRL 180
QY 121 KWRKRIIEKQPOSPKAPAPPPILKFNRPILFDYVRSSTADLDGLPLTHKKRL 180
Db 121 KWRKRIIEKQPOSPKAPAPPPILKFNRPILFDYVRSSTADLDGLPLTHKKRL 180
QY 181 TDEFRBPSTGKTCPLKALNLSNGRNDTIPVLIDIAERTGNMRZFINSPPFDIYYRQT 240
Db 181 TDEFRBPSTGKTCPLKALNLSNGRNDTIPVLIDIAERTGNMRZFINSPPFDIYYRQT 240
QY 241 ALHIAIERCKHYVELVAQADVHAQARGFPQKDEGYPYFGEPLSLAAGTNOPIH 300
Db 241 ALHIAIERCKHYVELVAQADVHAQARGFPQKDEGYPYFGEPLSLAAGTNOPIH 300
QY 301 VNYLTENPHKKAQDMRQDSRGNTVLAHVAIADNTRENTKPYTKYDILLKCARLPDS 360
Db 301 VNYLTENPHKKAQDMRQDSRGNTVLAHVAIADNTRENTKPYTKYDILLKCARLPDS 360
QY 361 NLEAVLNNDGSLPMMAAATGKIGFOHIIREVTDEBTRHLSRKFQDMAYGPVYSSLYD 420
Db 361 NLEAVLNNDGSLPMMAAATGKIGFOHIIREVTDEBTRHLSRKFQDMAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEIIVYNSKIENHHEMLAVEPINELRDKMRKFGASFTINAVSYIC 480
Db 421 LSSLDTCGEASVLEIIVYNSKIENHHEMLAVEPINELRDKMRKFGASFTINAVSYIC 480
QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNIKDLFMKCGPV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNIKDLFMKCGPV 540
QY 541 NSLFDGSPQLLYFYISVLYVSAALYAGIBAYLAVMVFALVGMNNAIYFTGKLXLTG 600
Db 541 NSLFDGSPQLLYFYISVLYVSAALYAGIBAYLAVMVFALVGMNNAIYFTGKLXLTG 600
QY 601 TYSIMIQILFKDLFRFLVYLFMIGYASALVSLNFCANMKCNEDQNTCTVPTPASC 660
Db 601 TYSIMIQILFKDLFRFLVYLFMIGYASALVSLNFCANMKCNEDQNTCTVPTPASC 660
QY 661 RDSEFTSFLLDLFKLITGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
Db 661 RDSEFTSFLLDLFKLITGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720
QY 721 TVGVSKESKHIWKLQ 736
Db 721 TVGVSKESKHIWKLQ 736

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RESULT 10

Q9ERZ7 PRELIMINARY; PRT; 873 AA.

AC Q9ERZ7, 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Vanilloid receptor-related osmotically activated channel.

ON Name=Trpv4; Synonyms=Vroac;  
 NS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=20531888; PubMed=11081638;  
 RA Liedtke W.B., Clloe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,  
 RA Sali A., Hudecpeh A.J., Friedman J.M., Heller S.;  
 RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a  
 RL candidate vertebrate osmoreceptor.";  
 RL Cell 103:525-535(2000).  
 DR EMBL; AF263552; AAC8028.1; -.  
 DR MED; MGI:1926945; Trpv4.  
 DR GO; GO:0005262; P:calcium channel activity; IDA.  
 DR GO; GO:0005034; F:osmosensor activity; IDA.  
 DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.  
 DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.  
 DR GO; GO:0047444; P:regulation of response to osmotic stress; IMP.  
 DR GO; GO:0030103; P:vasopressin secretion; IMP.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat channel\_TrpL.  
 DR InterPro; IPR008996; CytoK\_IL1\_likc.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR01768; TRPVRECEPTOR.  
 DR PRINTS; PR01769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 Transport.  
 SEQ SEQUENCE 873 AA; 98596 MW; 5DD87C92712B242A CRC64;

Query Match	94.2%	Score 3636;	DB 2;	Length 873;
Best Local Similarity	94.4%	Pred. No. 6.3e-221;		
Matches 697; Conservative	17;	Mismatches 22;	Indels 2;	Gaps 2

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QY  MADSSGPGAGGEVAELGDGSGTGGGAFPLSSIANLFEEDLSLSBVA-DWSKVG 59
DB  1 MADPGGPAALAGEVAEPDGSSTGCGBAFLSSIANLFEGESSSYFEPWMTASRPAG 60
QY  60 PEDGGRNLMKF-QGAFKGVNPIDLLESTLYESSVVGPKKAMPDLSFDVGYTRHSS 118
DB  61 PEDGGRNLMKKGSRSAFRKGVNPIDLLESTLYESSVVGPKKAMPDLSFDVGYTRHSS 120
QY  119 DKRRMRKKTIEKOPOSPAPAPPPILKVENRPIFLDIVSRGSTDLDGLLPFLTHKK 178
DB  121 DKRRMRKKEVQOSPAPAPPPILKVENRPIFLDIVSRGSTDLDLDGLSLFLTHKK 180
QY  179 RLTFEEFREPSTGKTCLPKALNLSGRNDTLPVLIDIAERTGNMREFINSFPRDIYRG 238
DB  181 RLTFEEFREPSTGKTCLPKALNLSGRNDTLPVLIDIAERTGNMREFINSFPRDIYRG 240
QY  239 QFALHIAIERCKHYVELLVAQADVHAQGRFFQPKDGGFTFYGELPLSLAACTNQP 298
DB  241 QFSIHIAIERCKHYVELLVAQADVHAQGRFFQPKDGGFTFYGELPLSLAACTNQP 300
QY  299 HLYNYITENPHKKADMRQDSRGNTYLAHVAIADTRENTRYKVTOMYOLLILLCARLPP 358
DB  301 HLYNYITENPHKKADMRQDSRGNTYLAHVAIADTRENTRYKVTOMYOLLILLCARLPP 360
QY  359 DSNLEAVLNDDGSLPLMAAKTGKIGFOHIIKREYTDDETRLSRKFQDMAGAPYSSSL 418
DB  361 DSNLEAVLNDDGSLPLMAAKTGKIGFOHIIKREYTDDETRLSRKFQDMAGAPYSSSL 420

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Qy	419	YDLSSLDTCGERASVLAETIAVYNSKIKENHEMLAEPINELLRDQMRKGVSPYINVS	478
Db	421	YDLSSLDTCGERASVLAETIAVYNSKIKENHEMLAEPINELLRDQMRKGVSPYINVS	480
Qy	479	LCAMVFTLTAYYOPLEGTPPYRYRTVDYRLAGEVITLFTGVLEFFETNIKOLFMKCP	538
Db	481	LCAMVFTLTAYYOPLEGTPPYRYRTVDYRLAGEVITLFTGVLEFFETNIKOLFMKCP	540
Qy	539	GVNSLEFIDSFOLLLEYISVLYVSAAVYLAGIEAVYAVWFALVIGMNAALFTTRGLK	598
Db	541	GVNSLEFIDSFOLLLEYISVLYVSAAVYLAGIEAVYAVWFALVIGMNAALFTTRGLK	600
Qy	599	TGTYSIMICKILFKDLFRPLVYLLFMIGYASALVSLNPMANAKVGNEDQNTQVTPP	658
Db	601	TGTYSIMICKILFKDLFRPLVYLLFMIGYASALVSLNPMANAKVGNEDQNTQVTPP	660
Qy	659	SCGDSSTFSTFLILDYFKLTIQMGDLEMLSTCYPVFILLVYIILFTVYLLNMLTALM	718
Db	661	ACRDSSTFSAFLILDYFKLTIQMGDLEMLSAKYPVVFILLVYIILFTVYLLNMLTALM	720
Qy	719	GETVGVQVSKESKHIINLKQ 736	
Db	721	GETVGVQVSKESKHIINLKQ 738	

RESULT 11	
Q96RS7	
ID	Q96RS7
AC	Q96RS7
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-MAR-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 26, Last annotation update)
DE	Vanilloid receptor-like protein 2.
CN	Name=VRL2;
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]

Query Match	90.0%;	Score 3472;	DB 2;	Length 803;
Best Local Similarity	100.0%;	Pred. No. 1.3e-210;		
Matches 668;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

69 MKEGGAERKGVNPIDLLSTLYESSVYGPKKAMPDSLFDYGYVRRHSHSDNKRWRKII 128



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Db      1 MFGQAFKRGVNPIDLESTLYESSVGPGEAPKAPMDSLFDYGTGRHSSDNKRRKTI 60
Qy      129 EKQPOSPPKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRLTDEEPRP 188
Db      61 EKQPOSPPKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRLTDEEPRP 120
Qy      189 STGKTCPLKALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIDYRGCTALHAIER 248
Db      121 STGKTCPLKALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIDYRGCTALHAIER 180
Qy      249 RCKHVEVLVAQGAADVHAQARGFQPKDEGGYFFGELPLSLAAGTQPHIVNLTENP 308
Db      181 RCKHVEVLVAQGAADVHAQARGFQPKDEGGYFFGELPLSLAAGTQPHIVNLTENP 240
Qy      309 HKKADMRRODSRGNTVLAHVLAADNTRENTKFTVMYDILLLKCARLPDSNLEAVLN 368
Db      241 HKKADMRRODSRGNTVLAHVLAADNTRENTKFTVMYDILLLKCARLPDSNLEAVLN 300
Qy      369 DGLSPILMAAATGKTGIFQHIIRREVTDEDTRHLSRKKRDMAVGPVSSLYDLSLDTG 428
Db      301 DGLSPILMAAATGKTGIFQHIIRREVTDEDTRHLSRKKRDMAVGPVSSLYDLSLDTG 360
Qy      429 BEASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYLCAMVIFTLT 488
Db      361 BEASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYLCAMVIFTLT 420
Qy      489 AAYPLSGTPEPPYRTTYDYLRLAGEVITLFTGVLFPPFNKIDLEMKKCPGVNSLFDIGS 548
Db      421 AAYPLSGTPEPPYRTTYDYLRLAGEVITLFTGVLFPPFNKIDLEMKKCPGVNSLFDIGS 480
Qy      549 FQLYFYISVYIVSALYLAGIEAYLAAMVPALVGMNALLFTRGKLTGTYSIMIQ 608
Db      481 FQLYFYISVYIVSALYLAGIEAYLAAMVPALVGMNALLFTRGKLTGTYSIMIQ 540
Qy      609 ILFDLRFPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPRYBSCRPSTST 668
Db      541 ILFDLRFPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPRYBSCRPSTST 600
Qy      669 FLIDLFLKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNMLALMGETVGOVSK 728
Db      601 FLIDLFLKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNMLALMGETVGOVSK 660
Qy      729 SKHIMKIQ 736
Db      661 SKHIMKIQ 668

RESULT 12
Q8NG64 PRELIMINARY; PRT; 811 AA.
AC Q8NG64;
DT 01-OCT-2002 (Tremblere, 22, Created)
DT 01-OCT-2002 (Tremblere, 22, Last sequence update)
DT 01-MAR-2004 (Tremblere, 26, Last annotation update)
DS CTRPCbeta cation channel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endochelium;
RA Xu F., Satoh E., Iijima T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB073669; BAC06573.1; -;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005261; P:cation channel activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat channel TrpL.
DR InterPro: IPR008996; Cytok rll like.
DR InterPro: IPR005821; Ion_trans.

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DR InterPro: IPR008347; Vanil_receptor.
DR InterPro: IPR008348; Vanil_receptor2.
DR Pfam: PF00023; Ank; 3.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR01415; ANKRIN.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR PRINTS: PR01769; VRL2RECEPTOR.
DR SMART: SM00248; ANK; 3.
DR PROSITE: PS00088; ANK_REPEAT; 1.
DR PROSITE: PS02977; ANK_REPEAT_REGION; 1.
DR ANK Repeat; Ion transport; Ionic channel; Transmembrane; Transport.
DR SEQUENCE 811 AA; 91220 MW; 38470FD07830781 CRC64;

Query Match
  89.8%; Score 3466; DB 2; Length 811;
  Best Local Similarity 91.6%; Pred No. 3,1e-210; Indels 60; Gaps 1;
  Matches 674; Conservative 0; Mismatches 2;

Qy      1 MADSEGRAPGGEVAILPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADASRPAGP 60
Db      1 MADSEGRAPGGEVAILPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADASRPAGP 60
Qy      61 GDGRPNLPMKFGAPKGVNPIDLESTLYESSVGPGEAPKAPMDSLFDYGTGRHSSDN 120
Db      61 GDGRPNLPMKFGAPKGVNPIDLESTLYESSVGPGEAPKAPMDSLFDYGTGRHSSDN 120
Qy      121 KRWKKIIEKOPSPKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRL 180
Db      121 KRWKKIIEKOPSPKAPAPPPILKVFNRPIILFDIVSRGSTADLDGLPLPLTHKKRL 180
Qy      181 TDEEFREPSGTCTCLPALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIDYRGCT 240
Db      181 TDEEFREPSGTCTCLPALINLSNGRNDTIPVLLDIAERTGNRRPINSPPRIDYRGCT 240
Qy      241 ALHAIERRCHYVELLVAQGAADVHAQARGFQPKDEGGYFFGELPLSLAAGTQPHI 300
Db      241 ALHAIERRCHYVELLVAQGAADVHAQARGFQPKDEGGYFFGELPLSLAAGTQPHI 300
Qy      301 VNYLTENPHKKADRRDSDRGNTVLAHVLAADNTRENTKFTVMYDILLLKCARLPDS 360
Db      301 VNYLTENPHKKADRRDSDRGNTVLAHVLAADNTRENTKFTVMYDILLLKCARLPDS 360
Qy      361 NLEAVLNNDGLSPILMAAATGKTGIFQHIIRREVTDEDTRHLSRKKRDMAVGPVSSLYD 420
Db      361 NLEAVLNNDGLSPILMAAATGKTGIFQHIIRREVTDEDTRHLSRKKRDMAVGPVSSLYD 420
Qy      421 LSSLDTCGEASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYLC 480
Db      421 LSSLDTCGEASVLEILVYNSKIENHEMLAABEPINELLRDKRRKGAVSFYINVSYLC 480
Qy      481 AMVIFTLTAYYOPLEGTPPYRTTYDYLRLAGEVITLFTGVLFPPFNKIDLEMKKCPGV 540
Db      421 AMVIFTLTAYYOPLEGTPPYRTTYDYLRLAGEVITLFTGVLFPPFNKIDLEMKKCPGV 480
Qy      541 NSLFDIGSPQLYFYISVYIVSALYLAGIEAYLAAMVPALVGMNALLFTRGKLTGT 600
Db      481 NSLFDIGSPQLYFYISVYIVSALYLAGIEAYLAAMVPALVGMNALLFTRGKLTGT 540
Qy      601 TYSIMIOKILPKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPRYBSC 660
Db      541 TYSIMIOKILPKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPRYBSC 600
Qy      661 RDESEFSTPLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNMLALMGE 720
Db      601 RDESEFSTPLDLFKLTIGMDLEMLSTKYPVVFIIILVTYIIILFVLLNMLALMGE 660
Qy      721 TVGQVSKESGHIMKIQ 736
Db      661 TVGQVSKESGHIMKIQ 676

RESULT 13
Q91XR5 PRELIMINARY; PRT; 803 AA.

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AC 091XR5;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Vanilloid receptor-like protein 2.  
 GN Name=Trpv4; Synonyms=Vrl2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Derst C., Schafer M.K.;  
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
 DB EMBL; AF279672; AK69486.1; -  
 DB MGI; MGI:1926945; Trpv4.  
 DR GO; GO:0005262; F:calcium channel activity; IEA.  
 DR GO; GO:0005034; F:osmosensor activity; IEA.  
 DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.  
 DR GO; GO:0007231; P:osmosensory signaling pathway; IEA.  
 DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.  
 DR GO; GO:0030103; P:vasopressin secretion; IMP.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_TrpL.  
 DR InterPro; IPR008996; CytoK\_IL1\_like.  
 DR InterPro; IPR005821; Ion trans-  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PRO1415; ANKTRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR PRINTS; PRO1769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_RRP\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.  
 SQ SEQUENCE 803 AA; 91438 MW; 79A5BD9323300029 CRC64;  
 Query Match 87.8%; Score 3389; DB 2; Length 803;  
 Best Local Similarity 96.6%; Pred. No. 2,2e-205;  
 Matches 645; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

DB 361 EEVSVEILVYNSKIENRHEMLAVEPINELIRDKRRKRGAVSFYINVSICAMVITLT 420  
 QY 489 AAYQPLEGTPPYPRRTVDYLRLAGEVITTFGYLFFFTNIKDLPMKKCPGNSLFDGS 548  
 DB 421 AAYQPLGTPPYPRRTVDYLRLAGEVITTFGYLFFFTSIKDLFTKCPGNSLFDGS 480  
 QY 549 FQLYPIYSVLVYSALYLAGIFAYLAVVAFVLCGMNLYFTRGKLTGYSIMIQK 608  
 DB 481 FQLYPIYSVLVYSALYLAGIFAYLAVVAFVLCGMNLYFTRGKLTGYSIMIQK 540  
 QY 609 ILFDLFRFLVLYLPMIGYASALVSLNPCANNKVCNEDQNTCTVTPYPSCRDSEFTST 668  
 DB 541 ILFDLFRFLVLYLPMIGYASALVSLNPCANNKVCNEDQNTCTVTPYPSCRDSEFTSA 600  
 QY 669 FLDDLFKLITGMGLMELSTKYPVVFILVYIILTFVLLNMLTLMGETVGOYSKE 728  
 DB 601 FLDDLFKLITGMGLMELSTKYPVVFILVYIILTFVLLNMLTLMGETVGOYSKE 660  
 QY 729 SKIWKIQ 736  
 DB 661 SKIWKIQ 668  
 RESULT 14  
 ID Q9DF53 PRELIMINARY; PRT; 852 AA.  
 AC Q9DF53;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Vanilloid receptor-related osmotically activated channel protein.  
 GN Name=VR-ONC;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxId=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cochlea;  
 RX MEDLINE=20531888; PubMed=11081638;  
 RA Liedtke W., Choe Y., Marti-Renom M.A., Bell A.N., Denis C.S., Sali A.,  
 Hudspeth A.J., Friedman J.M., Heller S.;  
 DE "Vanilloid receptor-related osmotically activated channel (VR-ONC), a  
 candidate vertebrate osmoreceptor.";  
 RT Cell 103:525-535(2000).  
 RL EMBL; AF261883; AAG28026.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; C:integral channel activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006812; F:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_TrpL.  
 DR InterPro; IPR008996; CytoK\_IL1\_like.  
 DR InterPro; IPR005821; Ion trans-  
 DR InterPro; IPR002016; Peroxidase.  
 DR InterPro; IPR001865; Ribosomal\_S2.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PRO1415; ANKTRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR PRINTS; PRO1769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_RRP\_REGION; 1.  
 DR PROSITE; PS500436; PEROXIDASE\_2; UNKNOWN\_1.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; UNKNOWN\_1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.

SQ SEQUENCE 852 AA; 96197 MW; E85365D3FAD08C1 CRC64;  
 Query Match 85.1%; Score 3284; DB 2; Length 852;  
 Best Local Similarity 86.5%; Pred. No. 1e-198;  
 Matches 624; Conservative 43; Mismatches 50; Indels 4; Gaps 2;

QY 17 ELPGDESTPGGEAFPLSLANLPGEGDGLSPSPADASR-PAGPGRPNLRMKFGQAF 75  
 DB 5 EDPDADGVDLDDSDPLSLANLPEVED---TPSPAEPSPRPGAGDKQMLRMKFGAF 61  
 QY 76 RKGVPNPIDLLESTLYESSVVPKPKAMPDSLFDVGTGRHSSDNKRKKKIIKQPS 135  
 DB 62 RKGPKPMELLESSTLYESSVVPKPKAMPDSLFDVGTGRHSSDNKRKKKIIKQPS 121  
 QY 136 KAPAPQPPPLIKVFNRPILFDIVSGSTADLDGLPFLTHKKRLTDEEPSTGKTC 195  
 DB 122 KGPAPNPPLIKVFNRPILFDIVSGSTADLDGLPFLTHKKRLTDEEPSTGKTC 181  
 QY 196 PKALINLSGNDITPVLADIAERTGNMRETFSPFDIYRGOTAHIAIERCKHYE 255  
 DB 182 PKALINLSGNDITPVLADIAERTGNMRETFSPFDIYRGOTAHIAIERCKHYE 241  
 QY 256 LIVAAGADVHAQAGRFEPKDEGGYFPGELPLISLAACNPHIYVLTENPHKADMR 315  
 DB 242 LIVAAGADVHAQAGRFEPKDEGGYFPGELPLISLAACNPHIYVLTENPHKADMR 301  
 QY 316 RODSRGNVTHALVAIADNTRENTKFTVYKMDLLKCARLPPSPNEAVLNDSPLM 375  
 DB 302 RODSRGNVTHALVAIADNTRENTKFTVYKMDLLKCARLPPSPNEAVLNDSPLM 361  
 QY 376 MAATGKIGIFQHIIRREVDDETRHLSRKKKMAVGPVYSLYDSSLDTGGEASVLE 435  
 DB 362 MAATGKIGIFQHIIRREVDDETRHLSRKKKMAVGPVYSLYDSSLDTGGEASVLE 421  
 QY 436 ILVNSKLENRHEMLAEPINELRDKMRKGAVSFTINVSYSICANVIFLTATYQPLE 495  
 DB 422 ILVNSKLENRHEMLAEPINELRDKMRKGAVSFTINVSYSICANVIFLTATYQPLE 481  
 QY 496 GTPPYPTVTVLRLAGEVITLFTGVLPFTNIKDLFMKKCPGVNSLFDIGSPQLYFI 555  
 DB 482 GTPPYPTVTVLRLAGEVITLFTGVLPFTNIKDLFMKKCPGVNSLFDIGSPQLYFI 541  
 QY 556 YSVLVYSALVYLAGIAYAVWFAVYLGMAALYTRGKLTGTYSIMIOKILFDOLF 615  
 DB 542 YSVLVYSALVYLAGIAYAVWFAVYLGMAALYTRGKLTGTYSIMIOKILFDOLF 601  
 QY 616 RFLVYLLFMIGVASALVSLINPCANMKVCNEDQNCVPTYPSCRDSSEPFLLDLFK 675  
 DB 602 RFLVYLLFMIGVASALVSLINPCANMKVCNEDQNCVPTYPSCRDSSEPFLLDLFK 661  
 QY 676 LTIIGMDLEMLSTKCEVVFILLYVYIILTFVLLNMLTALMGETVGOVSKSKHMKL 735  
 DB 662 LTIIGMDLEMLSTKCEVVFILLYVYIILTFVLLNMLTALMGETVGOVSKSKHMKL 721  
 QY 736 Q 736  
 DB 722 Q 722

## RESULT 15

OBOEN9 PRELIMINARY; PRT; 843 AA.  
 AC OBOEN9;  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 OS Vanilloid receptor-like protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Dorsal root ganglia;  
 RX MEDLINE=21842900; PubMed=11853675;  
 RA Jourd S.E., Julius D.,  
 RT "Molecular basis for species-specific sensitivity to 'hot' chill  
 peptide".  
 RL Cell 108:421-430(2002).  
 DR EMBL; AY072909; AAL78069.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; F:cation channel activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat channel\_TripL.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PRO1415; ANKYRIN.  
 DR PRINTS; PRO1768; TRP-RECEPTOR.  
 DR SMART; SM00248; ANK; 4.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.  
 SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 41.6%; Score 1604.5; DB 2; Length 843;  
 Best Local Similarity 47.5%; Pred. No. 1.2e-97;  
 Matches 343; Conservative 126; Mismatches 164; Indels 67; Gaps 16;

QY 41 EGBDGLSPSPADASRPAGPGRPLRMKFGAERKGVNPIDLLESTLY--ESSVVP 98  
 DB 27 DGEDSAL--ETAD-----GTYRHSNDKRRKKIIEKQ---QSPAPAPQPPIL 146  
 QY 99 ---PKRPMNSLDY-----GTYRHSNDKRRKKIIEKQ---QSPAPAPQPPIL 146  
 DB 65 DCDKMAPMDSFQOMDHMAPSVYKPHANRGRKHLTDSITGSEKRA-----F 116  
 QY 147 KVENRPLFDIVSRGSTADLDGLPFLTHKKRLTDEEPSTGKTCPLKALINLSGR 206  
 DB 117 KFYDRRIIPAVARGSTKDLDDLILYLRKLKHLTDEEPSTGKTCPLKALINLSGR 176  
 QY 207 NDTIPLVLADIAERTGNMRETFSPFDIYRGOTAHIAIERCKHYVELVAQADVHA 266  
 DB 177 NDTIPLVLADIAERTGNMRETFSPFDIYRGOTAHIAIERCKHYVELVAQADVHA 236  
 QY 267 QARGRFQRP-KDGGYVYFELPLSLAACNPHIYVLTENPHKADMRQDSRGTVL 325  
 DB 237 QARGRFQRP-KDGGYVYFELPLSLAACNPHIYVLTENPHKADMRQDSRGTVL 295  
 QY 326 HALVALADNTRENTKFTVYKMDLLKCARLPPSPNEAVLNDSPLMAATGKIGI 385  
 DB 296 HALVALADNTRENTKFTVYKMDLLKCARLPPSPNEAVLNDSPLMAATGKIGI 355  
 QY 386 FQHIIRREVDDETRHLSRKKKMAVGPVYSLYDSSLDTGGEASVILVNSKLEN 445  
 DB 356 FQHIIRREVDDETRHLSRKKKMAVGPVYSLYDSSLDTGGEASVILVNSKLEN 414  
 QY 446 RHEMLAVEPINEELRDKMRKGAVSFTINVSYSICANVIFLTATYQPLE--GTPPY- 502  
 DB 415 RHEMLAVEPINEELRDKMRKGAVSFTINVSYSICANVIFLTATYQPLE--GTPPY- 474  
 QY 503 RTVDYLRLAGVITLFTGVLPFTNIKDLFMKKCPGVNSLFDIGSPQLYFTYSVVI 562  
 DB 475 HSGVGFRTVLTGLSTVGGIYFFFRIGQ-YFVGRRSIKTLIVDSYSEVTFPHSHLLLS 533  
 QY 563 SAALVYLAGIAYAVWFAVYLGMAALYTRGKLTGTYSIMIOKILFDOLFLLVYL 622

```

Db      534  SVVLYFCGQELIYASWVFSIALGNANMLYTRGFQOMGIYSVMIAKMLIRDLCRMFYYL 593
QY      623  LFMIGYASATVSLINPCANMKVCNEDQ-TNCTVPTYPSCRDSETEST-----FLDLF 674
Db      594  VFLIGFSTAVVTLIED-----DNEGQDTNS--FYACSHTKRGRTSYNSLYTCLFLF 645
QY      675  KLITGMGDLMLSSIKYPPVFIIILVTYIILTFVILLMLIALMGETVGVSKESKHIWK 734
Db      646  KFTIGMGDLFPTENYRFKSVFVILLVLYVILLTYIILLNMLIALMGETVSKIAQESKSIWK 705
QY      735  LQ 736
Db      706  LQ 707

```

Search completed: December 2, 2004, 22:26:45  
 Job time : 206 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:36:21 ; Search time 43 Seconds  
(without alignments)  
1660.299 Million cell updates/sec

Title: US-10-090-215-12

Sequence: 1 MADSSRGPRAGFGEVAFPLPG.....GVVSKSKHIMKLGSGRRLL 742

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: 1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	2.2	838	2	T09054
2	16	2.2	839	2	JC7621
3	8	1.1	79	2	H58933
4	8	1.1	143	2	F95116
5	8	1.1	143	2	D97985
6	8	1.1	213	2	A56152
7	8	1.1	213	2	AC3408
8	8	1.1	252	1	H69002
9	8	1.1	286	2	C64538
10	8	1.1	334	2	A12150
11	8	1.1	341	2	AE2445
12	8	1.1	379	2	A85130
13	8	1.1	379	2	G98000
14	8	1.1	484	2	F71317
15	8	1.1	496	2	T44987
16	8	1.1	550	2	C86348
17	8	1.1	618	2	A75469
18	8	1.1	688	2	H83070
19	8	1.1	723	2	UC7795
20	8	1.1	725	2	UC7531
21	8	1.1	727	2	JC7796
22	8	1.1	1454	2	T13709
23	7	0.9	31	2	S00685
24	7	0.9	55	2	E81500
25	7	0.9	80	2	B69157
26	7	0.9	90	2	H87544
27	7	0.9	96	2	T28327
28	7	0.9	111	2	H72707
29	7	0.9	117	2	I38362

#### ALIGNMENTS

30	7	0.9	122	2	H70176	hypothetical prote
31	7	0.9	138	2	S59128	trp-like protein -
32	7	0.9	145	1	J00947	atrial natriuretic
33	7	0.9	147	2	A37763	virid protein - Ag
34	7	0.9	147	2	AC3250	viridA/G regulated p
35	7	0.9	149	2	S06883	virid protein - Ag
36	7	0.9	160	2	S59129	trp-1ike protein -
37	7	0.9	170	2	D75388	NADH2 dehydrogenas
38	7	0.9	170	2	T08348	hypothetical prote
39	7	0.9	178	2	S76780	hypothetical prote
40	7	0.9	179	2	AE2225	hypothetical prote
41	7	0.9	195	2	B97050	guanylate kinase (
42	7	0.9	207	2	AF0199	probable lipoprote
43	7	0.9	210	2	AF3192	two component resp
44	7	0.9	222	2	F82420	arginine ABC trans
45	7	0.9	224	2	F84239	hypothetical prote

#### RESULT 1

T09054  
capsaicin receptor - rat  
N:Alternate names: vanilloid receptor subtype 1  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
R:Accession: T09054  
R:Category: M.J.; Schumacher, M.A.; Tomimaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D  
Nature 389, 816-824, 1997  
A:Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.  
A:Reference number: Z16539; MUID:98007969; PMID:9349813  
A:Accession: T09054  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-838 <CAT>  
A:Cross-references: UNIPROT:Q35433; EMBL:AF029310; NID:92570932; PIDD:AC53398.1; PIDD:G  
A:Experimental source: dorsal root ganglion  
C:Keywords: ion channel; receptor

Query Match 2.2%; Score 16; DB 2; Length 838;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 282 FFFGELPLSLAAGTNO 297  
Db 245 FFFGELPLSLAAGTNO 260

#### RESULT 2

JC7621  
capsaicin receptor, VR1 - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
R:Accession: JC7621  
R:Category: D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.  
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001  
A:Title: The tissue distribution and functional characterization of human VR1.  
A:Reference number: JC7621; MUID:21139751; PMID:11243859  
A:Contents: Dorsal root ganglia  
A:Accession: JC7621  
A:Molecule type: mRNA  
A:Residues: 1-839 <COR>  
A:Cross-references: UNIPROT:Q9H304; GB:AF196175  
C:Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a  
its integrative activation by several noxious stimuli, and plays an important role in i  
C:Genetics:  
A:Gene: vr1  
A:Map position: 17p13  
C:Keywords: transmembrane protein  
F:201-233/Domain: ankyrin #status predicted <ANK1>  
F:248-280/Domain: ankyrin #status predicted <ANK2>  
F:333-365/Domain: ankyrin #status predicted <ANK3>

F:433-455/Domain: transmembrane #status predicted <TM1>  
F:477-495/Domain: transmembrane #status predicted <TM2>  
F:508-531/Domain: transmembrane #status predicted <TM3>  
F:543-569/Domain: transmembrane #status predicted <TM4>  
F:578-597/Domain: transmembrane #status predicted <TM5>  
F:624-644/Region: pore loop #status predicted  
F:656-684/Domain: transmembrane #status predicted <TM6>

Query Match 2.2%; Score 16; DB 2; Length 839;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLACTNQ 297  
DB 246 FYFGEPLSLACTNQ 261

## RESULT 3

H58933  
succinate dehydrogenase hydrophobic subunit - Cyanidioschyzon merolae mitochondrion  
C:Species: mitochondrion Cyanidioschyzon merolae  
C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: H58933

R:Ohta, N.; Sato, N.; Kuroiwa, T.  
Nucleic Acids Res. 26, 5190-5198, 1998  
A:Title: Structure and organization of the mitochondrial genome of the unicellular red alga Cyanidioschyzon merolae  
A:Reference number: A58930, MUID:99030526; PMID:9801318  
A:Accession: H58933

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <ARN>  
A:Cross-references: UNIPROT:Q9Z2N2; GB:D89861; NID:94115781; PIDN:BAA36542.1; PID:dl0375

C:Genetics:  
A:Gene: sdhD  
A:Genome: mitochondrion  
C:Keywords: mitochondrion

Query Match 1.1%; Score 8; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 FLIVVILF 624  
DB 72 FLIVVILF 79

## RESULT 4

F95116  
Gtra family protein [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: F95116

R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Hickey, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Kadane, D.; Holtapple, neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000, MUID:21357209; PMID:11463916

A:Accession: F95116  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-143 <KUR>  
A:Cross-references: UNIPROT:Q97R28; GB:AE005672; PIDN:AAK75127.1; PID:914972484; GSPDB:C

A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP1011

Query Match 1.1%; Score 8; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 STFLDLF 674

DB 85 STFLDLF 92

## RESULT 5

mesh protease [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: D97986

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Ee, R.; LeBlanc, D.J.; Lee, L.N.; Letkovitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.  
Y. J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: D97986  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-143 <KUR>  
A:Cross-references: UNIPROT:Q8DQ02; GB:AE007317; PIDN:AAK9720.1; PID:915458524; GSPDB:C

C:Genetics:  
A:Gene: mesh

Query Match 1.1%; Score 8; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 STFLDLF 674  
DB 85 STFLDLF 92

## RESULT 6

A56152  
major 25k outer membrane protein precursor - Brucella abortus  
C:Species: Brucella abortus  
C>Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: A56152

R:de Wergifosse, P.; Lintermans, P.; Linnec, J.N.; Cloeckaert, A.  
J. Bacteriol. 177, 1911-1914, 1995  
A:Title: Cloning and nucleotide sequence of the gene coding for the major 25-kilodalton  
A:Reference number: A56152, MUID:95204367; PMID:7896724

A:Accession: A56152  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-213 <DEA>  
A:Cross-references: UNIPROT:Q44664; GB:X79284; NID:9769744; PIDN:CAA5872.1; PID:9769745

Query Match 1.1%; Score 8; DB 2; Length 213;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 LVIVSAL 566  
DB 7 LVIVSAL 14

## RESULT 7

AC3408  
25k outer-membrane immunogenic protein precursor [imported] - Brucella melitensis (strain 25k)  
C:Species: Brucella melitensis  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:Accession: AC3408

R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova, J.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leticia, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688

A:Accession: AC3408  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-213 <KUR>  
 A:Cross-references: UNIPROT:Q45321; GB:AE008917; PIDN:AAL52430.1; PID:G17983234; GSPDB:G  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BME11249  
 A:Map position: 1

Query Match 1.1%; Score 8; DB 2; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 8.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 559 LVIYSAL 566  
 DB 7 LVIYSAL 14

RESULT 8  
 H69002  
 conserved hypothetical protein MTH1019 - Methanobacterium thermoautotrophicum (strain De  
 C:Species: Methanobacterium thermoautotrophicum  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Dec-2002  
 C:Accession: H69002  
 R:Smith, D.R.; Doucette-Stramm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
 K., S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
 A:Reference number: A69000; MUID:98037514; PMID:9371463  
 A:Accession: H69002  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-252 <MTH>  
 A:Cross-references: GB:AE000874; GB:AE000666; NID:G2622110; PIDN:AAB85515.1; PID:G262212  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH1019  
 C:Superfamily: uncharacterized conserved protein

Query Match 1.1%; Score 8; DB 1; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 214 LDIAERTG 221  
 DB 68 LDIAERTG 75

RESULT 9  
 C64538  
 cytochrome-c oxidase (EC 1.9.3.1) chain fixp - Helicobacter pylori (strain 26695)  
 C:Species: Helicobacter pylori  
 C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
 C:Accession: C64538  
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khakhria, H.G.; Glodek, A.; McKenna  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Deliman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
 Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A:Reference number: A64520; MUID:97394467; PMID:9252185  
 A:Accession: C64538  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-286 <TOM>  
 A:Cross-references: UNIPROT:Q24958; GB:AE000536; GB:AE000511; NID:G2313230; PIDN:AAD0721  
 C:Superfamily: cytochrome c oxidase, cbh3-type, fixp subunit, cytochrome c6 homology  
 C:Keywords: chromoprotein; electron transfer; heme; iron; membrane-associated complex; m  
 F:128/132/Binding site: heme (Cys) (covalent) #status predicted  
 F:133/Binding site: heme iron (His) (axial ligand) #status predicted  
 F:219/222/Binding site: heme (Cys) (covalent) #status predicted  
 F:223/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 1.1%; Score 8; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KALNLSN 204  
 DB 278 KALNLSN 285

RESULT 10  
 A12150  
 serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: A12150  
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: A12150  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-334 <KUR>  
 A:Cross-references: UNIPROT:Q8YTF7; GB:BA000019; PIDN:BAW74459.1; PID:G17131853; GSPDB  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: al12760

Query Match 1.1%; Score 8; DB 2; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 432 SVLETLIVY 439  
 DB 129 SVLETLIVY 136

RESULT 11  
 AE2445  
 hypothetical protein alr5117 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AE2445  
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AE2445  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-341 <KUR>  
 A:Cross-references: UNIPROT:Q8YV24; GB:BA000019; PIDN:BAW76816.1; PID:G17134255; GSPDB:  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr5117  
 C:Superfamily: alcohol dehydrogenase, long-chain alcohol dehydrogenase homology

Query Match 1.1%; Score 8; DB 2; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ELPISTIA 293  
 DB 136 ELPISTIA 143

RESULT 12  
 A95130  
 glycogen biosynthesis protein GlgD [imported] - Streptococcus pneumoniae (strain TIGR4)  
 C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
 C/Accession: A95130  
 R/Retireltn, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held  
 on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
 mon, T.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001  
 A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
 A/Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.  
 A/Reference number: A95000; MIMD:21357209; PMID:11463916  
 A/Accession: A95130  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-379 <KUR>  
 A/Cross-references: UNIPROT:Q97086; GB:AE005672; PIDN:AAK75234.1; PID:G14972600; GSPDB:Q  
 C/Genetics:  
 A/Experimental source: strain TIGR4  
 A/Gene: SP1123

Query Match 1.1%; Score 8; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 FPLSSIAN 38  
 Db 42 FPLSSIAN 49

RESULT 13  
 G98000  
 required for glycocon biosynthesis [imported] - *Streptococcus pneumoniae* (strain R6)  
 C/Species: *Streptococcus pneumoniae*  
 C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
 C/Accession: G98000  
 R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; DeHoff, B.S.; E  
 y, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McHenry, S.; M  
 y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
 A/Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.  
 A/Reference number: A97872; MIMD:21429245; PMID:11544234  
 A/Accession: G98000  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-379 <KUR>  
 A/Cross-references: UNIPROT:Q9BDP4; GB:AE007317; PIDN:AAK99835.1; PID:G15458649; GSPDB:Q  
 C/Genetics:  
 A/Gene: g19D

Query Match 1.1%; Score 8; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 FPLSSIAN 38  
 Db 42 FPLSSIAN 49

RESULT 14  
 F71317  
 probable antigen, p83/100 - syphilis spirochete  
 C/Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: F71317  
 R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
 reon, J.; Khakak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDc  
 they, L.; Weidman, U.; Smith, H.O.; Venter, J.C.  
 Science 281, 375-388, 1998  
 A/Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.  
 A/Reference number: A71250; MIMD:9832770; PMID:9665876  
 A/Accession: F71317  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-484 <COL>

A/Cross-references: UNIPROT:Q83499; GB:AE001225; GB:AE000520; NID:G3322775; PIDN:AAK6547  
 A/Experimental source: strain Nichols  
 C/Genetics:  
 A/Gene: TP0486

Query Match 1.1%; Score 8; DB 2; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 HALVALAD 333  
 Db 418 HALVALAD 425

RESULT 15  
 T44987  
 aldehyde dehydrogenase (EC 1.2.1.-) [imported] - *Haloflex volcanii* megaplasmid pHV3  
 C/Species: *Haloflex volcanii*  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
 C/Accession: T44987  
 R/Farahani, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois, R.L.  
 submitted to the EMBL Data Library, March 1997  
 A/Description: Hereditary instability of the megaplasmid pHV3, and filamentation in the  
 A/Reference number: Z22886  
 A/Accession: T44987  
 A/Status: preliminary; translated from GB/EMBL/DDBI  
 A/Molecule type: DNA  
 A/Residues: 1-496 <FAR>  
 A/Cross-references: UNIPROT:Q34184; EMBL:U95374; PIDN:AAK71806.1  
 A/Experimental source: strain DS2  
 C/Genetics:  
 A/Map position: megaplasmid pHV3  
 A/Gene: plasmid  
 A/Note: expressed during exponential growth  
 C/Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology  
 C/Keywords: oxidoreductase

Query Match 1.1%; Score 8; DB 2; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GSTRADLDG 168  
 Db 360 GSTRADLDG 367

Search completed: December 2, 2004, 22:46:26  
 Job time: 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:27:41 ; Search time 203 Seconds

(without alignments)  
2103.094 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 742  
Sequence: 1 MADSEGRAPGGEVADLPG.....GQVSKSKHIMLQSGRRRL 742

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	736	99.2	853 2	Q86YZ6
2	736	99.2	871 2	Q8NDY7
3	736	99.2	871 2	Q9HBCO
4	736	99.2	871 2	Q96C92
5	668	90.0	803 2	Q96RS7
6	635	85.6	871 2	Q9HBA0
7	384	51.8	811 2	Q8NG64
8	181	24.4	871 2	Q9ERZ8
9	112	15.1	803 2	Q91XR5
10	112	15.1	871 2	Q9EPK8
11	112	15.1	871 2	Q9ERZ4
12	112	15.1	871 2	Q9RS76
13	112	15.1	873 2	Q9ERZ7
14	68	9.2	852 2	Q9DF53
15	28	3.8	852 2	Q9Z182
16	19	2.6	103 2	Q8RET8
17	19	2.6	195 2	Q9SLU9
18	19	2.6	765 2	Q8NET9
19	19	2.6	790 2	Q8NDW7
20	19	2.6	790 2	Q8NFW7
21	19	2.6	791 2	Q8NFW8
22	19	2.6	791 2	Q8NFW8
23	16	2.2	468 2	Q8K424
24	16	2.2	511 2	Q9Z0B4
25	16	2.2	778 2	Q9H303
26	16	2.2	838 2	Q9UM56
27	16	2.2	838 2	Q9UM57
28	16	2.2	839 2	Q8NER1
29	16	2.2	839 2	Q9NC74
30	16	2.2	839 2	Q9NY22
31	16	2.2	839 2	Q9H0G9

32	16	2.2	839 2	Q9H304	Q9H304 homo sapien
33	16	2.2	839 2	Q6R5A3	Q6R5A3 cavia porce
34	16	2.2	839 2	Q704Y3	Q704Y3 mus musculu
35	16	2.2	839 2	Q8K1W1	Q8K1W1 cavia porce
36	16	2.2	839 2	AA513460	AA513460 cavia por
37	16	2.2	839 2	CA055661	CA055661 mus muscu
38	16	2.2	839 2	BAD20301	BAD20301 mus muscu
39	16	2.2	842 2	Q6RX08	Q6RX08 oryctolagus
40	16	2.2	842 2	AA344558	AA344558 oryctolag
41	16	2.2	843 2	Q8QFN9	Q8QFN9 gallus gall
42	14	1.9	151 2	Q81Z19	Q81Z19 homo sapien
43	14	1.9	471 2	Q9JLM0	Q9JLM0 rattus norv
44	14	1.9	756 2	Q6JGX2	Q6JGX2 f-11 rat/mo
45	14	1.9	756 2	Q9WTR1	Q9WTR1 mus musculu

## ALIGNMENTS

RESULT 1					
Q86YZ6		PRELIMINARY:	PRT:	853 AA.	
AC	Q86YZ6				
DT	01-JUN-2003 (TREMBLrel. 24, Created)				
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Hypothetical protein TRPV-SV.				
GN	Name=TRPV-SV.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI Taxid=9606;				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RL	Suzuki S.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Suzuki M.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, AB100308; BAC55864.1; --.				
DR	GO; GO:0016021; C:Integral to membrane; IEA.				
DR	GO; GO:0005261; F:cation channel activity; IEA.				
DR	GO; GO:0006812; P:cation transport; IEA.				
DR	InterPro: IPR002110; Cat. channel Trpl.				
DR	InterPro: IPR008996; CytoK_IL1_like.				
DR	InterPro: IPR005821; Ion trans.				
DR	InterPro: IPR004729; TRPChannel.				
DR	InterPro: IPR008347; Vanil_receptor.				
DR	InterPro: IPR008348; Vanil_receptor2.				
DR	Pfam: PF00023; Ank; 3.				
DR	Pfam: PF00520; Ion_trans; 1.				
DR	PRINTS: PR01415; ANKTRIN.				
DR	PRINTS: PR01768; TRPVRECEPTOR.				
DR	PRINTS: PR01769; VRL2RECEPTOR.				
DR	SMART: SM00248; ANK; 3.				
DR	TIGRFAMs: TIGR00870; trp; 1.				
DR	PROSITE: PS50088; ANK_REPEAT; 1.				
DR	PROSITE: PS50297; ANK_REPEAT_REGION; 1.				
KW	ANK repeat; Hypothetical protein; Ion transport; Ionic channel;				
KW	Transmembrane; Transport.				
SQ	SEQUENCE 853 AA; 96448 MW; EAA07196606AED20 CRC64;				
Query Match	99.2%; Score 736; DB 2; Length 853;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches	736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MADSEGRAPGGEVADLPGDESGTPGGEAPFLSIANIPEGDSGLSPSPADARPGP 60				
DB	1 MADSEGRAPGGEVADLPGDESGTPGGEAPFLSIANIFGDSGLSPSPADARPGP 60				
QY	61 GDGRNLRMKFGAERKGVNPFIDLLSTYESSVVPKPKAPMDSLFDYGTGRHSSDN 120				

[illegible]

Query	Match	99.2%	Score 736;	DB 2;	Length 871;	
Best Local Similarity	100.0%	Pred. NO. 0;				
Matches	736;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
DR	GO: GO:0004872; F:receptor activity; IEA.					
DR	GO: GO:0006812; P:cation transport; IEA.					
DR	InterPro: IPR002110; ANK.					
DR	InterPro: IPR002111; Cat channel_TypL.					
DR	InterPro: IPR008996; Cytok_IL1_like.					
DR	InterPro: IPR005821; Ion trans.					
DR	InterPro: IPR004729; TRP channel.					
DR	InterPro: IPR008347; Vanil_receptor.					
DR	InterPro: IPR008348; Vanil_receptor2.					
DR	Pfam; PF00023; Ank; 3.					
DR	Pfam; PF00520; Ion_trans; 1.					
DR	PRINTS; PRO1415; ANKRYN.					
DR	PRINTS; PRO1768; TREVRECEPTOR.					
DR	PRINTS; PRO1769; VRL2RECEPTOR.					
DR	SMART; SM00248; ANK; 3.					
DR	TIGRFAMs; TIGR00870; trp; 1.					
DR	PROSITE; PS50088; ANK_REPEAT; 1.					
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.					
DR	ANK_repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.					
DR	SEQUENCE	871 AA;	98280 MW;	C62056B86C5A6FB6	CRC64;	
QY	1	MADSEGGPRAGPGGVAELPGDESGTGGGEAPPLSLANLFGEDGSLSPSPADASRPAGP	60			
DB	1	MADSEGGPRAGPGGVAELPGDESGTGGGEAPPLSLANLFGEDGSLSPSPADASRPAGP	60			
QY	61	GDGPPNLRMKQGAFRKGVNPPIDLBESTLYESSVPEPKAPMDSLFDYGYTHHSSDN	120			
DB	61	GDGPPNLRMKQGAFRKGVNPPIDLBESTLYESSVPEPKAPMDSLFDYGYTHHSSDN	120			
QY	121	KRWKKKIIIEKQOPAKPAAPQPPILTKYENRPIIFDIYSRGSSTADLDGLPFLTHKKRL	180			
DB	121	KRWKKKIIIEKQOPAKPAAPQPPILTKYENRPIIFDIYSRGSSTADLDGLPFLTHKKRL	180			
QY	181	TDEEFPREBSTGKTCLPKALNLSNGRNDTIPVLLDIAERTGNMREFFINSPPRIDYYRGQT	240			
DB	181	TDEEFPREBSTGKTCLPKALNLSNGRNDTIPVLLDIAERTGNMREFFINSPPRIDYYRGQT	240			
QY	241	ALHIAIERCKHAYEILVAQADVHAQGRFPQPDGSGYFPEGELSLSLAAGTNOPI	300			
DB	241	ALHIAIERCKHAYEILVAQADVHAQGRFPQPDGSGYFPEGELSLSLAAGTNOPI	300			
QY	301	VNYLTLENHKKADMRQDSRGNTVLAALVAIADNTRENTKFTVXYDILLKCARLPDS	360			
DB	301	VNYLTLENHKKADMRQDSRGNTVLAALVAIADNTRENTKFTVXYDILLKCARLPDS	360			
QY	361	NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDENTRHLSRKFKOMAGPYVSSLYD	420			
DB	361	NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDENTRHLSRKFKOMAGPYVSSLYD	420			
QY	421	LSLSDTGEESAVALIILVNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVSYL	480			
DB	421	LSLSDTGEESAVALIILVNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVSYL	480			
QY	481	AMVIFTLTAYYQPILEGTPPYRTTYVTLRLAGEYITLFTGYLPEFTNLIKDLFMKKCPV	540			
DB	481	AMVIFTLTAYYQPILEGTPPYRTTYVTLRLAGEYITLFTGYLPEFTNLIKDLFMKKCPV	540			
QY	541	NSLFDGSGFOLLYFYFYSVLVISAALYAGIEAYLAVWVFLVLCOMNALYTRRGKLTG	600			
DB	541	NSLFDGSGFOLLYFYFYSVLVISAALYAGIEAYLAVWVFLVLCOMNALYTRRGKLTG	600			
QY	601	TYSIMIQKILPKDLFRPLVYLPMIGASALVSLNFCANMKVCNEOCTNCTVTPYPSG	660			
DB	601	TYSIMIQKILPKDLFRPLVYLPMIGASALVSLNFCANMKVCNEOCTNCTVTPYPSG	660			
QY	661	RDSEFFSFELLDLPELTLTGMGIDLEMLSTKXPPVYVLIILVYIILTFVLLNMLALMGE	720			
DB	661	RDSEFFSFELLDLPELTLTGMGIDLEMLSTKXPPVYVLIILVYIILTFVLLNMLALMGE	720			

QY 721 TVGVSKSKSHIWKIQ 736  
 DB 721 TVGVSKSKSHIWKIQ 736

## RESULT 3

Q9HBCO PRELIMINARY; PRT; 871 AA.  
 AC Q9HBCO; 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE ORPc4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Renal cortex;  
 RX MEDLINE=20482174; PubMed=11025659;  
 RA Strickman R., Harteneck C., Nunnemacher K., Schultz G., Plant T.D.;  
 RT "OTPC4, a nonselective cation channel that confers sensitivity to  
 extracellular osmolarity."  
 RL Nat. Cell Biol. 2:695-702(2000).  
 DR EMBL, AF258465; AAG16127.1; -.  
 DR GO; GO:0016021; C:integral to membrane; NAS.  
 DR GO; GO:0015281; F:nonselective cation channel activity; NAS.  
 DR GO; GO:0006816; P:calcium ion transport; NAS.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_Trip.  
 DR InterPro; IPR008896; Cytok\_IL1\_like.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PRO1415; ANKYRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR PRINTS; PRO1769; VRL2RECEPTOR.  
 DR SMART; SMO0248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR KEGG; KEGG:00000; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 871 AA; 98294 MW; C62056B86DEA6F86 CRC64;

Query Match 99.2%; Score 736; DB 2; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSSEPRAGPAGVAELPGDESGTPGGEAFPLSLANTFEGEGSLSPPSADSRAPG 60  
 DB 1 MADSSSEPRAGPAGVAELPGDESGTPGGEAFPLSLANTFEGEGSLSPPSADSRAPG 60  
 QY 61 GDGPRNLRMKFQGAERKGVNPDIDLSTLYESSVVGPKKAPMDSLFDTYGRHSSDN 120  
 DB 61 GDGPRNLRMKFQGAERKGVNPDIDLSTLYESSVVGPKKAPMDSLFDTYGRHSSDN 120  
 QY 121 KRMKKKIIKQPOGPKAPAPPPPIILVFNNPILFDIVSRGSTDLDGLLPFLTHKKRL 180  
 DB 121 KRMKKKIIKQPOGPKAPAPPPPIILVFNNPILFDIVSRGSTDLDGLLPFLTHKKRL 180  
 QY 181 TDEEFPSTGTCTLPALNLSGRNDTTPVLIDIERGNMSEFINSPPRDIYYGQT 240  
 DB 181 TDEEFPSTGTCTLPALNLSGRNDTTPVLIDIERGNMSEFINSPPRDIYYGQT 240  
 QY 241 ALHAIERRCKHYVELLVAQADVAQARGFPQPKDGGGYFYFGLPLSLAQTNPPI 300  
 DB 241 ALHAIERRCKHYVELLVAQADVAQARGFPQPKDGGGYFYFGLPLSLAQTNPPI 300

QY 301 VNYLTENPKKADMRRODSRGNTVLAVALADNTRNTKFTYMYDILLKCARLPDS 360  
 DB 301 VNYLTENPKKADMRRODSRGNTVLAVALADNTRNTKFTYMYDILLKCARLPDS 360  
 QY 361 NLEAVLNDGSLPIMAAATGKIGIFQHIIRBVDDETRHLSRKKDMAYGVSYSLYD 420  
 DB 361 NLEAVLNDGSLPIMAAATGKIGIFQHIIRBVDDETRHLSRKKDMAYGVSYSLYD 420  
 QY 421 LSLDTCGEASVLELVNNSKIENRHEMLAEPINELLROKWRKGAVSFYINVSYL 480  
 DB 421 LSLDTCGEASVLELVNNSKIENRHEMLAEPINELLROKWRKGAVSFYINVSYL 480  
 QY 481 AMVIFTLAYYQPLGEPPEPYRTTYDYLRLAGEVITLFTGYLFFPTNKDLPMKKCPGV 540  
 DB 481 AMVIFTLAYYQPLGEPPEPYRTTYDYLRLAGEVITLFTGYLFFPTNKDLPMKKCPGV 540  
 QY 541 NSLFTDGSFOLLYFYISLVIVSALVLAGIRAYLAWVFALVGMNVALFTRGKLTLG 600  
 DB 541 NSLFTDGSFOLLYFYISLVIVSALVLAGIRAYLAWVFALVGMNVALFTRGKLTLG 600  
 QY 601 TYSIMIOKILFMDLFRFLVYLLFMIGYASALVSLNRCANMKVCNEDQTNCTVPYPSG 660  
 DB 601 TYSIMIOKILFMDLFRFLVYLLFMIGYASALVSLNRCANMKVCNEDQTNCTVPYPSG 660  
 QY 661 RDSERTSTFLDLFLITIGMDLEMLSTKYPPVFIILVTYIILFTVLLNMLTALMGE 720  
 DB 661 RDSERTSTFLDLFLITIGMDLEMLSTKYPPVFIILVTYIILFTVLLNMLTALMGE 720  
 QY 721 TVGVSKSKSHIWKIQ 736  
 DB 721 TVGVSKSKSHIWKIQ 736

## RESULT 4

Q96G92 PRELIMINARY; PRT; 871 AA.  
 AC Q96G92;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Vanilloid receptor like channel-2.  
 GN Name=VRL-2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ishibashi K.;  
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB032427; BAB69040.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; F:cation channel activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_Trip.  
 DR InterPro; IPR008966; Cytok\_IL1\_like.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PRO1415; ANKYRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR PRINTS; PRO1769; VRL2RECEPTOR.  
 DR SMART; SMO0248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.

SQ SEQUENCE 871 AA; 98266 MW; C62056A401ECA8B6 CRC64;  
 Query Match 99.2%; Score 736; DB 2; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MADSEGRAGGAEVLEPGDESGTGGGEAFPLSLANLPEGEDSLSPSPADSRPAGP 60
DB 1 MADSEGRAGGAEVLEPGDESGTGGGEAFPLSLANLPEGEDSLSPSPADSRPAGP 60
OY 61 GDRGNLMMKFGAERKGVNPIDILESTLYESSVVPQPKAPMDSLFDYGYRHHSSDN 120
DB 61 GDRGNLMMKFGAERKGVNPIDILESTLYESSVVPQPKAPMDSLFDYGYRHHSSDN 120
OY 121 KMRKKIIEKQPSKAPAPPPILKYFNRPLIDIVSRGSTADLDGLPLTHKKRL 180
DB 121 KMRKKIIEKQPSKAPAPPPILKYFNRPLIDIVSRGSTADLDGLPLTHKKRL 180
OY 121 KMRKKIIEKQPSKAPAPPPILKYFNRPLIDIVSRGSTADLDGLPLTHKKRL 180
DB 121 KMRKKIIEKQPSKAPAPPPILKYFNRPLIDIVSRGSTADLDGLPLTHKKRL 180
OY 181 TDEFRPSTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREPIINSPPRDIYRGQT 240
DB 181 TDEFRPSTGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREPIINSPPRDIYRGQT 240
OY 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDGGYFYFGEPLSLAAGTNOPIH 300
DB 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDGGYFYFGEPLSLAAGTNOPIH 300
OY 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDGGYFYFGEPLSLAAGTNOPIH 300
DB 241 ALHAIERRCKHYVELVAQADVAHQARGFPOPKDGGYFYFGEPLSLAAGTNOPIH 300
OY 301 VNYLTENPKKADMRRODSRGNTVLAIVAIADNTRKNTKVTMVDLLKCARLPDPS 360
DB 301 VNYLTENPKKADMRRODSRGNTVLAIVAIADNTRKNTKVTMVDLLKCARLPDPS 360
OY 361 NLEAVLNDGSLPLMMAAKTGKIGIFQHIIRREVTEDETRHLSRKKDWAYGVPVSSLYD 420
DB 361 NLEAVLNDGSLPLMMAAKTGKIGIFQHIIRREVTEDETRHLSRKKDWAYGVPVSSLYD 420
OY 421 IASLDTCGEASVLELTVNSKIENHEMLAVEPINELRDKRRKGAVSFYINVSYC 480
DB 421 IASLDTCGEASVLELTVNSKIENHEMLAVEPINELRDKRRKGAVSFYINVSYC 480
OY 481 ANVIFLTVAYOPELSTPPYRTTVDYRIAGEVITLFTGVLPFTNKKDLPKMKCPGV 540
DB 481 ANVIFLTVAYOPELSTPPYRTTVDYRIAGEVITLFTGVLPFTNKKDLPKMKCPGV 540
OY 541 NSLFDIGSPQLYFISVAVISAALYLAGIEAVLAVMVFALVGMNMLYFTRGKLTG 600
DB 541 NSLFDIGSPQLYFISVAVISAALYLAGIEAVLAVMVFALVGMNMLYFTRGKLTG 600
OY 601 TVSIMIQKILFKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
DB 601 TVSIMIQKILFKDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSC 660
OY 661 RDESTSTFLDIPKLTIGMDLEMLSTKYPVFIIILVTYIILFVLLANMLALMGE 720
DB 661 RDESTSTFLDIPKLTIGMDLEMLSTKYPVFIIILVTYIILFVLLANMLALMGE 720
OY 721 TVGQVSKESKHIWKLQ 736
DB 721 TVGQVSKESKHIWKLQ 736
  
```

RP SEQUENCE FROM N.A.  
 RA Deret C., Schaefer M.K.,  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF279673; AAK69487.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; F:channel activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR Interpro; IPR002111; ANK.  
 DR Interpro; IPR002111; Cat channel TrpL.  
 DR Interpro; IPR008996; CytoK IL1 like.  
 DR Interpro; IPR004729; Ion trans-  
 DR Interpro; IPR008347; Vanil\_receptor.  
 DR Interpro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PRO1415; ANKYRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR PRINTS; PRO1769; VRLRRECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRFAMS; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW transport.  
 SQ SEQUENCE 803 AA; 91635 MW; AB329C595B325784 CRC64;

Query Match 90.0%; Score 668; DB 2; Length 803;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 69 MKFGAERKGVNPIDILESTLYESSVVPQPKAPMDSLFDYGYRHHSSDNKMRKKI 128
DB 1 MKFGAERKGVNPIDILESTLYESSVVPQPKAPMDSLFDYGYRHHSSDNKMRKKI 60
OY 129 EKQPSKAPAPPPILKYFNRPLIDIVSRGSTADLDGLPLTHKKRLDEFRBP 188
DB 61 EKQPSKAPAPPPILKYFNRPLIDIVSRGSTADLDGLPLTHKKRLDEFRBP 120
OY 189 STGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREPIINSPPRDIYRGQALHAIER 248
DB 121 STGKTCPLKALNLSNGRNDTIPVLDIAERTGNMREPIINSPPRDIYRGQALHAIER 180
OY 249 RCKHYVELVAQADVAHQARGFPOPKDGGYFYFGEPLSLAAGTNOPIHVNTEP 308
DB 181 RCKHYVELVAQADVAHQARGFPOPKDGGYFYFGEPLSLAAGTNOPIHVNTEP 240
OY 309 HKKADMRRODSRGNTVLAIVAIADNTRKNTKVTMVDLLKCARLPDPSNLEAVLN 368
DB 241 HKKADMRRODSRGNTVLAIVAIADNTRKNTKVTMVDLLKCARLPDPSNLEAVLN 300
OY 369 DGLSPLMMAAKTGKIGIFQHIIRREVTEDETRHLSRKKDWAYGVPVSSLYDLSLPTCG 428
DB 301 DGLSPLMMAAKTGKIGIFQHIIRREVTEDETRHLSRKKDWAYGVPVSSLYDLSLPTCG 360
OY 429 EASVLELTVNSKIENHEMLAVEPINELRDKRRKGAVSFYINVSYLCAWVIFLT 488
DB 361 EASVLELTVNSKIENHEMLAVEPINELRDKRRKGAVSFYINVSYLCAWVIFLT 420
OY 489 AAYOPELSTPPYRTTVDYRIAGEVITLFTGVLPFTNKKDLPKMKCPGVNSLFDGS 548
DB 421 AAYOPELSTPPYRTTVDYRIAGEVITLFTGVLPFTNKKDLPKMKCPGVNSLFDGS 480
OY 549 FOLLVPIYSVAVISAALYLAGIEAVLAVMVFALVGMNMLYFTRGKLTGYSIMIQ 608
DB 481 FOLLVPIYSVAVISAALYLAGIEAVLAVMVFALVGMNMLYFTRGKLTGYSIMIQ 540
OY 609 ILFDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSCRDSEFTST 668
DB 541 ILFDLFRPLVYLLFMIGYASALVSLNPCANMKVCNEDQNTCTVPTPSCRDSEFTST 600
OY 669 FLDDLFLTLTGMDLEMLSTKYPVFIIILVTYIILFVLLANMLALMGEIVGQVSK 728
  
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Db      601 FLDLFLKLTIGMDLMSSTKYPVVFILLVYIITLVLLNMLIALMGSTVQVSKS 660
Qy      729 SKHIMKLQ 736
Db      661 SKHIMKLQ 668

RESULT 6
Q9HBA0
AC      Q9HBA0
ID      Q9HBA0;
AC      Q9HBA0;
DT      01-MAR-2001 (Tremblrel. 16, Created)
DT      01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT      01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE      Vanilloid receptor-related osmotically activated channel.
DN      Name=VROAC;
OS      Homo sapiens (Human);
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20531888; PubMed=11081638;
RA      Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA      Sait A., Hudspeth A.J., Friedman J.M., Heller S.;
RT      "Vanilloid receptor-related osmotically activated channel (VR-ORC), a
RT      candidate vertebrate osmoreceptor.";
RL      Cell 103:525-535(2000).
DR      EMBL; AF263523; AAC28029.1; -
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005261; F:cation channel activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006812; P:cation transport; IEA.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR002111; Cat channel TrpL.
DR      InterPro; IPR008996; CytoK_IL1_like.
DR      InterPro; IPR005821; Ion trans.
DR      InterPro; IPR004729; TRPChannel.
DR      InterPro; IPR008347; Vanil_receptor.
DR      InterPro; IPR008348; Vanil_receptor2.
DR      Pfam; PF00023; Ank; 3.
DR      Pfam; PF00520; Ion trans; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      PRINTS; PR01768; TRPVRECEPTOR.
DR      PRINTS; PR01769; VRL2RECEPTOR.
DR      SMART; SM00248; ANK; 3.
DR      TIGRFAms; TIGR00870; trp; 1.
DR      PROSITE; PS50088; ANK_REPEAT; 1.
DR      PROSITE; PS50297; ANK_REGION; 1.
KW      ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW      transport.
SQ      SEQUENCE 871 AA; 98265 MW; A86F6BEC9103C19 CRC64;

Query Match      85.6%; Score 635; DB 2; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      241 ALHAIERRCKHYVELVAQADVAQAQGRFFOPDEGGYFYPGELPLSLAAGTNOPIH 300
Db      241 ALHAIERRCKHYVELVAQADVAQAQGRFFOPDEGGYFYPGELPLSLAAGTNOPIH 300
Qy      301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKPYTKMYDILLKCARLPPOS 360
Db      301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKPYTKMYDILLKCARLPPOS 360
Qy      361 NLEAVLNDGSLPLMAAKTKIGIFQHIIRREVTDETRHLSRPFKMAVGPVYSSLYD 420
Db      361 NLEAVLNDGSLPLMAAKTKIGIFQHIIRREVTDETRHLSRPFKMAVGPVYSSLYD 420
Qy      421 LSLDTCGEASVLEIIVYNSKIENRHMVAEPINELRDWRKFGAVSFYINVSVC 480
Db      421 LSLDTCGEASVLEIIVYNSKIENRHMVAEPINELRDWRKFGAVSFYINVSVC 480
Qy      481 AMVIFTLTAVYQPLEGTPPYRTVDYLRAGEVITLFTGVLFETNIKDLFMKKCEGV 540
Db      481 AMVIFTLTAVYQPLEGTPPYRTVDYLRAGEVITLFTGVLFETNIKDLFMKKCEGV 540
Qy      541 NSLFLDGSFQILYFYSVLVVSALYLAGIAYAVVFPALVGMNALYFTRGKLTG 600
Db      541 NSLFLDGSFQILYFYSVLVVSALYLAGIAYAVVFPALVGMNALYFTRGKLTG 600
Qy      601 TYSIMIOKILPKDLFRFLVYLIFMIGYASALVSLNCAVMKVCNEDQNTVPTPSC 660
Db      601 TYSIMIOKILPKDLFRFLVYLIFMIGYASALVSLNCAVMKVCNEDQNTVPTPSC 660
Qy      661 RDSEFTSTLLDLFKLTIGMDLMSSTKYPVVFILLVYIITLVLLNMLIALMG 720
Db      661 RDSEFTSTLLDLFKLTIGMDLMSSTKYPVVFILLVYIITLVLLNMLIALMG 720
Qy      721 TVGQVSKSKHIMKLQ 736
Db      721 TVGQVSKSKHIMKLQ 736

RESULT 7
Q9HBA0
AC      Q9HBA0;
ID      Q9HBA0;
AC      Q9HBA0;
DT      01-OCT-2002 (Tremblrel. 22, Created)
DT      01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT      01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE      OTRPCbeta cation channel.
OS      Homo sapiens (Human);
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      TISSUE=heart; endotheilium;
RA      Xu F., Satoh E., Iijima T.;
RL      Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB073669; BAC06573.1; -
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005261; F:cation channel activity; IEA.
DR      GO; GO:0006812; P:cation transport; IEA.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR002111; Cat channel TrpL.
DR      InterPro; IPR008996; CytoK_IL1_like.
DR      InterPro; IPR005821; Ion trans.
DR      InterPro; IPR008347; Vanil_receptor.
DR      InterPro; IPR008348; Vanil_receptor2.
DR      Pfam; PF00023; Ank; 3.
DR      Pfam; PF00520; Ion trans; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      PRINTS; PR01768; TRPVRECEPTOR.
DR      PRINTS; PR01769; VRL2RECEPTOR.
DR      SMART; SM00248; ANK; 3.
DR      PROSITE; PS50088; ANK_REPEAT; 1.
DR      PROSITE; PS50297; ANK_REGION; 1.

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ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.  
KW SEQUENCE 811 AA; 91220 MW; 3847D0FD07830781 CRC64;

Query Match 51.8%; Score 384; DB 2; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADSSGPRAGPGGVAELPGDESGPGGEAPPLSLANLPGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGGVAELPGDESGPGGEAPPLSLANLPGEDGSLSPSPADASRPAGP 60
QY 61 GDGPRNLAMKQGAARFKVGNPIDLLESTLYESSVVPKKAQMDSLFDYGYTHHSSDN 120
DB 61 GDGPRNLAMKQGAARFKVGNPIDLLESTLYESSVVPKKAQMDSLFDYGYTHHSSDN 120
QY 121 KRWKRTIEKQPGSKAPAPQPPPLIKTPNRPILFDIYRSRGTADLGLPLLTHKKRL 180
DB 121 KRWKRTIEKQPGSKAPAPQPPPLIKTPNRPILFDIYRSRGTADLGLPLLTHKKRL 180
QY 121 KRWKRTIEKQPGSKAPAPQPPPLIKTPNRPILFDIYRSRGTADLGLPLLTHKKRL 180
DB 121 KRWKRTIEKQPGSKAPAPQPPPLIKTPNRPILFDIYRSRGTADLGLPLLTHKKRL 180
QY 181 TDEFRPSTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREPIINSPPEDIYRQGT 240
DB 181 TDEFRPSTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREPIINSPPEDIYRQGT 240
QY 241 ALHIAIERCKHYVELLVAQADVAHQARGFQPKDEGGYFYFGLPLSLAATNOPIH 300
DB 241 ALHIAIERCKHYVELLVAQADVAHQARGFQPKDEGGYFYFGLPLSLAATNOPIH 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTKMYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTKIG 384
DB 361 NLEAVLNNDGSLPLMAAKTKIG 384
```

## RESULT 8

Q9ERZ8 PRELIMINARY; PRT; 871 AA.

```
AC 09ERZ8;
DT 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN Name-Vracc.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=20511888; PubMed=11081618;
RA Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RU Cell 103:525-535(2000).
DR EMBL; AF263521; MAG28027.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR008996; Cytok_IL1_Ilike.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK_3.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01768; TRPVRECEPTOR.
```

PRINTS; PR01769; VRL2RECEPTOR.

DR SMART; SM00248; ANK\_3.  
DR TIGRFAMs; TIGR00870; trip\_1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
KW Transport.

QY SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;  
Query Match 24.4%; Score 181; DB 2; Length 871;  
Best Local Similarity 100.0%; Pred. No. 5,9e-171;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 173 LITHKKRLTDEFRPSTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREPIINSPP 232
DB 173 LITHKKRLTDEFRPSTGKTCPLKALINLSNGRNDTIPVLIDIAERTGNMREPIINSPP 232
QY 233 DIYRGQTAHIALERRCKHYVELLVAQADVAHQARGFQPKDEGGYFYFGLPLSLA 292
DB 233 DIYRGQTAHIALERRCKHYVELLVAQADVAHQARGFQPKDEGGYFYFGLPLSLA 292
QY 293 ACTNPHIVNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTKMYDILLK 352
DB 293 ACTNPHIVNYLTENPHKADMRQDSRGNTVLAVALADNTRENTKFTKMYDILLK 352
QY 353 C 353
DB 353 C 353
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## RESULT 9

Q91XR5 PRELIMINARY; PRT; 803 AA.

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AC 091XR5;
DT 01-DEC-2001 (TREMELREL. 19, Created)
DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)
DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN Name=Trpv4; Synonyms=Vr12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Derst C., Schaefer M.K.;
RU Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279672; AK69486.1; -
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0005262; F:calcium channel activity; IEA.
DR GO; GO:0005034; F:osmosensor activity; IEA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IEA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0031003; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR008996; Cytok_IL1_Ilike.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK_3.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK_3.
DR TIGRFAMs; TIGR00870; trip_1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
```

KW Transport. 803 AA; 91438 MW; 79A5BD9323300029 CRC64;  
SEQUENCE

Query Match 15.1%; Score 112; DB 2; Length 803;  
Best Local Similarity 100.0%; Pred. No. 4.2e-102;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERCKHYVELVAQADVAHQAARGRFQPKDEGGYFYFGLPLSLAAGTNPHTV 301  
DB 174 LHAIERCKHYVELVAQADVAHQAARGRFQPKDEGGYFYFGLPLSLAAGTNPHTV 233  
QY 302 NYLTENPHKKADMRDORSRGNTVHALVAADNTRENTKFTTKMYDILLKLC 353  
DB 234 NYLTENPHKKADMRDORSRGNTVHALVAADNTRENTKFTTKMYDILLKLC 285

## RESULT 10

Q9EPK8 PRELIMINARY; PRT; 871 AA.  
AC Q9EPK8.  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Transient receptor potential protein 12.  
GN Name=Trpv4; Synonyms=Trp12;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=20547522; PubMed=11094154;  
RA Wiesenbach U., Boeding M., Freichel M., Flockert V.,  
RT "Trp12, a novel Trp related protein from kidney."  
RL FEBS Lett. 485:127-134(2000).  
DR EMBL; AJ296078; CAC20703.1; -.  
DR MGD; MGI:1926945; Trpv4.  
DR GO; GO:0005262; F:calcium channel activity; IDA.  
DR GO; GO:0005034; F:osmosensor activity; IDA.  
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.  
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.  
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.  
DR GO; GO:0030103; P:vasopressin secretion; IMP.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR002111; Cat channel Trpv.  
DR InterPro; IPR008996; CytoK\_IL1\_like.  
DR InterPro; IPR005821; Ion trans.  
DR InterPro; IPR004729; TRPChannel.  
DR InterPro; IPR008347; Vanil\_receptor.  
DR InterPro; IPR008348; Vanil\_receptor2.  
DR Pfam; PF00023; Ank; 3.  
DR Pfam; PF00520; Ion trans; 1.  
DR PRINTS; PRO1768; TRPVRECEPTOR.  
DR PRINTS; PRO1769; VRL2RECEPTOR.  
DR SMART; SM00248; ANK; 3.  
DR TIGRFAMs; TIGR00870; trp; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
KW Transport.  
SQ SEQUENCE 871 AA; 98026 MW; 5BAC5E33F89CEA05 CRC64;

Query Match 15.1%; Score 112; DB 2; Length 871;  
Best Local Similarity 100.0%; Pred. No. 4.5e-102;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERCKHYVELVAQADVAHQAARGRFQPKDEGGYFYFGLPLSLAAGTNPHTV 301  
DB 242 LHAIERCKHYVELVAQADVAHQAARGRFQPKDEGGYFYFGLPLSLAAGTNPHTV 301  
QY 302 NYLTENPHKKADMRDORSRGNTVHALVAADNTRENTKFTTKMYDILLKLC 353

DB 302 NYLTENPHKKADMRDORSRGNTVHALVAADNTRENTKFTTKMYDILLKLC 353

## RESULT 11

Q9EQZ4 PRELIMINARY; PRT; 871 AA.  
AC Q9EQZ4.  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Ion channel.  
GN Name=Trpv4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22692536; PubMed=12692122;  
RA Suzuki M., Mizuno A., Kodaira K., Imai M.,  
RT "Impaired pressure sensation in mice lacking TRPV4."  
RL J. Biol. Chem. 278:22664-22668(2003).  
DR EMBL; AB021875; BAA83731.2; -.  
DR MGD; MGI:1926945; Trpv4.  
DR GO; GO:0005262; F:calcium channel activity; IDA.  
DR GO; GO:0005034; F:osmosensor activity; IDA.  
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.  
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.  
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.  
DR GO; GO:0030103; P:vasopressin secretion; IMP.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR002111; Cat channel Trpv.  
DR InterPro; IPR008996; CytoK\_IL1\_like.  
DR InterPro; IPR005821; Ion trans.  
DR InterPro; IPR008347; Vanil\_receptor.  
DR InterPro; IPR008348; Vanil\_receptor2.  
DR Pfam; PF00023; Ank; 3.  
DR Pfam; PF00520; Ion trans; 1.  
DR PRINTS; PRO1768; TRPVRECEPTOR.  
DR PRINTS; PRO1769; VRL2RECEPTOR.  
DR SMART; SM00248; ANK; 3.  
DR TIGRFAMs; TIGR00870; trp; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.  
KW SEQUENCE 871 AA; 98060 MW; 3285A576D32DD95 CRC64;

Query Match 15.1%; Score 112; DB 2; Length 871;  
Best Local Similarity 100.0%; Pred. No. 4.5e-102;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIERCKHYVELVAQADVAHQAARGRFQPKDEGGYFYFGLPLSLAAGTNPHTV 301  
DB 242 LHAIERCKHYVELVAQADVAHQAARGRFQPKDEGGYFYFGLPLSLAAGTNPHTV 301  
QY 302 NYLTENPHKKADMRDORSRGNTVHALVAADNTRENTKFTTKMYDILLKLC 353  
DB 302 NYLTENPHKKADMRDORSRGNTVHALVAADNTRENTKFTTKMYDILLKLC 353

## RESULT 12

Q9ES76 PRELIMINARY; PRT; 871 AA.  
AC Q9ES76.  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE OTRPC4 cation channel.  
GN Name=Trpv4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVBV;
RX MEDLINE=20482174; PubMed=11025659;
RA Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
RT "ORPPLC, a nonselective cation channel that confers sensitivity to
   extracellular osmolarity."
RL Nat. Cell Biol. 2:695-702(2000).
DR EMBL; AF208026; AAG17543.1; -.
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:osmosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR008996; CytoK IL1 like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRP channel.
DR InterPro; IPR008347; Vanil receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK; 3.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01768; TRP RECEPTOR.
DR PRINTS; PR01769; VRL2 RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRfams; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
KW SEQUENCE 871 AA; 98069 MW; 2B28D554083F0DA CRC64;
SQ
Query Match 15.1%; Score 112; DB 2; Length 873;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIAERCKHYVELLVAGADVHAQARFPQDEGGYFFGELPLSLACTNPHIV 301
DB 242 LHAIAERCKHYVELLVAGADVHAQARFPQDEGGYFFGELPLSLACTNPHIV 301
QY 302 NYLTENPHKKADRRDSSRGNTVLAHVLAADNTRENTFVTKMYDILLK 353
DB 302 NYLTENPHKKADRRDSSRGNTVLAHVLAADNTRENTFVTKMYDILLK 353

RESULT 13
Q9ERZ7 PRELIMINARY; PRT; 873 AA.
ID Q9ERZ7
AC Q9ERZ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN Name=Trpv4; Synonyms=Vtrac;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=20531868; PubMed=11081638;
RA Hiedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
   candidate vertebrate osmoreceptor."
RL Cell 103:525-535(2000).
DR EMBL; AF263522; AAG28028.1; -.
DR MGD; MGI:1926945; Trpv4.

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DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR008996; CytoK IL1 like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRP channel.
DR InterPro; IPR008347; Vanil receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; ANK; 3.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01768; TRP RECEPTOR.
DR PRINTS; PR01769; VRL2 RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRfams; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
   Transport.
KW SEQUENCE 873 AA; 98596 MW; 5DD87C92712B24EA CRC64;
SQ
Query Match 15.1%; Score 112; DB 2; Length 873;
Best Local Similarity 100.0%; Pred. No. 4.5e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LHAIAERCKHYVELLVAGADVHAQARFPQDEGGYFFGELPLSLACTNPHIV 301
DB 244 LHAIAERCKHYVELLVAGADVHAQARFPQDEGGYFFGELPLSLACTNPHIV 303
QY 302 NYLTENPHKKADRRDSSRGNTVLAHVLAADNTRENTFVTKMYDILLK 353
DB 304 NYLTENPHKKADRRDSSRGNTVLAHVLAADNTRENTFVTKMYDILLK 355

RESULT 14
Q9DFS3 PRELIMINARY; PRT; 852 AA.
ID Q9DFS3
AC Q9DFS3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel protein.
GN Name=VR-OAC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cochlea;
RX MEDLINE=20531868; PubMed=11081638;
RA Hiedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
   candidate vertebrate osmoreceptor."
RL Cell 103:525-535(2000).
DR EMBL; AF261883; AAG28026.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR008996; CytoK IL1 like.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR001865; Ribosomal_S2.

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Search completed: December 2, 2004, 22:42:47  
 Job time : 206 secs

DR InterPro; IPR004729; TRPchannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PRO1415; ANKTRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR PRINTS; PRO1769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 3.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00436; PEROXIDASE\_2; UNKNOWN\_1.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; UNKNOWN\_1.  
 DR ANK\_repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.  
 SQ SEQUENCE 852 AA; 96197 MW; E85365D3FAD08C1 CRC64;

Query Match 9.2%; Score 68; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-58;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 558 EAYLAWVFALYLGMMNALYFRGLKLTGTYSIMIQKILFKDLFRPLVYLFPATGYASA 617  
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QY 632 LVSLNPC 639  
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 DB 618 LVSLNPC 625

## RESULT 15

Q92182 PRELIMINARY; PRT; 528 AA.  
 AC Q92182;  
 DT 01-MAY-1999 (TRENBLREL. 10, Created)  
 DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE Stretch-inhibitable nonselective channel (SIC).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=99156912; PubMed=10037722;  
 RA Suzuki M., Sato U., Katsuwada K., Ooki G., Imai M.;  
 RT "Cloning of a stretch-inhibitable nonselective cation channel.";  
 RL J. Biol. Chem. 274:6330-6335 (1999).  
 DR EMBL; AB015231; BA034942.2; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; P:cation channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_TyPL.  
 DR InterPro; IPR008996; CytoK\_IL1\_like.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR SMART; SM00248; ANK; 1.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 528 AA; 61017 MW; 93E4B00A6A231FD0 CRC64;

Query Match 3.8%; Score 28; DB 2; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 LILNMLIALMGRTVGVSKEKSHIMKQ 736  
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 DB 366 LILNMLIALMGRTVGVSKEKSHIMKQ 393

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GenCore version 5.1.6  
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OM protein - protein search, using BW model

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(without alignments)  
1200.194 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 742

Sequence: 1 MADSEGPRAAGPEVAELPG.....GVVSKSKHIVKLQSGRRRL 742

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size: 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Issued Patents AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	635	85.6	871	4	US-09-500-123-7
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4	16	2.2	511	4	US-09-667-422-5
5	16	2.2	838	3	US-09-235-451-2
6	16	2.2	838	4	US-09-132-316-3
7	16	2.2	838	4	US-09-667-422-9
8	16	2.2	838	4	US-09-978-303-2
9	16	2.2	839	3	US-09-197-636-2
10	16	2.2	839	3	US-09-197-636-4
11	16	2.2	839	3	US-09-197-636-8
12	16	2.2	839	3	US-09-235-451-34
13	16	2.2	839	4	US-09-533-230A-2
14	16	2.2	839	4	US-09-667-422-4
15	16	2.2	839	4	US-09-978-303-34
16	16	2.2	843	3	US-09-235-451-25
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18	14	1.9	71	3	US-09-235-451-14
19	14	1.9	71	3	US-09-978-303-14
20	14	1.9	761	3	US-09-235-451-4
21	14	1.9	761	4	US-09-978-303-4
22	14	1.9	764	3	US-09-235-451-36
23	14	1.9	764	4	US-09-978-303-36
24	14	1.9	889	4	US-09-132-316-2
25	11	1.5	727	3	US-09-235-451-23
26	11	1.5	727	4	US-09-978-303-23
27	10	1.3	34	4	US-09-149-476-624

28	10	1.3	57	3	US-09-235-451-15	Sequence 15, Appl
29	10	1.3	57	4	US-09-978-303-15	Sequence 15, Appl
30	9	1.2	428	4	US-09-252-991A-24452	Sequence 24452, A
31	8	1.1	84	4	US-09-248-796A-26822	Sequence 26822, A
32	8	1.1	97	3	US-08-858-207A-515	Sequence 515, App
33	8	1.1	114	4	US-09-270-767-42187	Sequence 42187, A
34	8	1.1	119	4	US-09-134-000C-4066	Sequence 4066, Ap
35	8	1.1	120	4	US-09-248-796A-24245	Sequence 24245, A
36	8	1.1	120	4	US-09-248-796A-27147	Sequence 27147, A
37	8	1.1	144	4	US-09-252-991A-16650	Sequence 16650, A
38	8	1.1	239	3	US-08-986-304-3	Sequence 3, Appl
39	8	1.1	337	4	US-09-252-991A-26243	Sequence 26243, A
40	8	1.1	337	4	US-09-107-532A-5998	Sequence 5998, Ap
41	8	1.1	379	4	US-09-583-110-3811	Sequence 3811, A
42	8	1.1	496	4	US-09-252-991A-17357	Sequence 17357, A
43	8	1.1	570	4	US-09-252-991A-20010	Sequence 20010, A
44	8	1.1	704	4	US-09-252-991A-30631	Sequence 30631, A
45	8	1.1	725	4	US-09-350-457A-2	Sequence 2, Appl

## ALIGNMENTS

## RESULT 1

US-09-500-123-12  
; Sequence 12, Application US/09500123  
; Patent No. 6455278  
; GENERAL INFORMATION:  
; APPLICANT: Dublin, Adrienne E  
; APPLICANT: Huvar, Arne  
; APPLICANT: Erlander, Mark G  
; APPLICANT: Glass, Charles A  
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor  
; TITLE OF INVENTION: VR3  
; FILE REFERENCE: Human VR3 receptors  
; CURRENT APPLICATION NUMBER: US/09/500,123  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 742  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-500-123-12

Query Match Best Local Similarity 100.0%; Score 742; DB 4; Length 742;

Matches 742; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GDGPRNLRKMGQAFRRKGVNPI	DLLESTLYESSVVPKPKAPMDSL	FDVGYRRHSSDN	120
DB	61	GDGPRNLRKMGQAFRRKGVNPI	DLLESTLYESSVVPKPKAPMDSL	FDVGYRRHSSDN	120
QY	121	KRWKKKIIIEKQSPKAPAPQPP	ILKFNRPILFDIVSRGSTADL	GLPFLTHKRL	180
DB	121	KRWKKKIIIEKQSPKAPAPQPP	ILKFNRPILFDIVSRGSTADL	GLPFLTHKRL	180
QY	181	TDEFRPSTGKTLPLALNTLSGR	NDTLPVLIDIAERTGMKEFINS	PRDIYRQOT	240
DB	181	TDEFRPSTGKTLPLALNTLSGR	NDTLPVLIDIAERTGMKEFINS	PRDIYRQOT	240
QY	241	ALHTAIRRCKHYVELLVAQADV	HAQARGFPQKDEGYFYGELPL	SLAAGTNOPI	300
DB	241	ALHTAIRRCKHYVELLVAQADV	HAQARGFPQKDEGYFYGELPL	SLAAGTNOPI	300
QY	301	VNYLTENPHKADRRDSDRGNT	TLHALVALADTRENTFVTQV	YDILLKCARLPDS	360
DB	301	VNYLTENPHKADRRDSDRGNT	TLHALVALADTRENTFVTQV	YDILLKCARLPDS	360

QY 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFQKMAVGPPVSSLYD 420  
DB 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFQKMAVGPPVSSLYD 420  
QY 421 LSSLDTCGEBAVSEILVYNSKIEHRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480  
DB 421 LSSLDTCGEBAVSEILVYNSKIEHRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480  
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DB 481 AMVIFTLTAAYQPLEGTPPYPRITVDYLRAGEVITLFTGVLFFPTINIKDLEFMKCKGV 540  
QY 541 NSLFDGSPOLLIFYYSVLVISAALYIAGIEAYIAVAVFALVIGMNNALYFTRGKLTG 600  
DB 541 NSLFDGSPOLLIFYYSVLVISAALYIAGIEAYIAVAVFALVIGMNNALYFTRGKLTG 600  
QY 601 TYSIMIOKILFEDLPFLVYLFLMIGYASALVSLNFCAMKVCNEDQTNCTVETPSC 660  
DB 601 TYSIMIOKILFEDLPFLVYLFLMIGYASALVSLNFCAMKVCNEDQTNCTVETPSC 660  
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DB 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVILLNMLIALMGE 720  
QY 721 TVGVSKSKSKHIMKIQSGRRRL 742  
DB 721 TVGVSKSKSKHIMKIQSGRRRL 742

## RESULT 2

US-09-500-123-7  
; Sequence 7, Application US/09500123  
; Patent No. 6455278  
; GENERAL INFORMATION:  
; APPLICANT: Dublin, Adrienne B  
; APPLICANT: Huvay, Arne  
; APPLICANT: Eriander, Mark G  
; APPLICANT: Glass, Charles A  
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor  
; TITLE OF INVENTION: VR3  
; FILE REFERENCE: Human VR3 receptors  
; CURRENT APPLICATION NUMBER: US/09/500,123  
; CURRENT FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 871  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-500-123-7

Query Match 85.6%; Score 635; DB 4; Length 871;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSGPPAGGEVAELPGDESGTPGGAFLPSLIANLFBGSDGSLSPADASRPAGP 60  
DB 1 MADSSGPPAGGEVAELPGDESGTPGGAFLPSLIANLFBGSDGSLSPADASRPAGP 60  
QY 61 GGRPLRMKPGGARPKGVNPIIDLESTLYESSVVPGRKAPMDSLPGYGYRRHSSDN 120  
DB 61 GGRPLRMKPGGARPKGVNPIIDLESTLYESSVVPGRKAPMDSLPGYGYRRHSSDN 120  
QY 121 KMRKKIIEKQSPAPAPOPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180  
DB 121 KMRKKIIEKQSPAPAPOPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180  
QY 181 TDEEPEESTGTCTCPKALINLSNGRNDTTPVLDIAERTGNMREPTNSPPFDIYYRGQT 240  
DB 181 TDEEPEESTGTCTCPKALINLSNGRNDTTPVLDIAERTGNMREPTNSPPFDIYYRGQT 240  
QY 241 AHHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFYFGEPLPSLAACNTQPHI 300  
DB 241 AHHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFYFGEPLPSLAACNTQPHI 300

DB 241 AHHIAIERCKHYVELLVAGADVHAQARGFPQPKDEGGYFYFGEPLPSLAACNTQPHI 300  
QY 301 VNYLTENHKTADMRQDSRGNTVLHAIVALADNTRENTKEVTKMYDILLKCARLFPDS 360  
DB 301 VNYLTENHKTADMRQDSRGNTVLHAIVALADNTRENTKEVTKMYDILLKCARLFPDS 360  
QY 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFQKMAVGPPVSSLYD 420  
DB 361 NLEAVLNNDGSLPLMAAKTGKIGIFOHIIIRREVTDEBTRHLSRKFQKMAVGPPVSSLYD 420  
QY 421 LSSLDTCGEBAVSEILVYNSKIEHRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480  
DB 421 LSSLDTCGEBAVSEILVYNSKIEHRHMLAVEPINELLRDKMRKFGAVSFYINVSYLIC 480  
QY 481 AMVIFTLTAAYQPLEGTPPYPRITVDYLRAGEVITLFTGVLFFPTINIKDLEFMKCKGV 540  
DB 481 AMVIFTLTAAYQPLEGTPPYPRITVDYLRAGEVITLFTGVLFFPTINIKDLEFMKCKGV 540  
QY 541 NSLFDGSPOLLIFYYSVLVISAALYIAGIEAYIAVAVFALVIGMNNALYFTRGKLTG 600  
DB 541 NSLFDGSPOLLIFYYSVLVISAALYIAGIEAYIAVAVFALVIGMNNALYFTRGKLTG 600  
QY 601 TYSIMIOKILFEDLPFLVYLFLMIGYASALVSLNFCAMKVCNEDQTNCTVETPSC 660  
DB 601 TYSIMIOKILFEDLPFLVYLFLMIGYASALVSLNFCAMKVCNEDQTNCTVETPSC 660  
QY 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVILLNMLIALMGE 720  
DB 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVEIILVTYIILTFVILLNMLIALMGE 720  
QY 721 TVGVSKSKSKHIMKIQ 736  
DB 721 TVGVSKSKSKHIMKIQ 736

## RESULT 3

US-09-500-123-9  
; Sequence 9, Application US/09500123  
; Patent No. 6455278  
; GENERAL INFORMATION:  
; APPLICANT: Dublin, Adrienne B  
; APPLICANT: Huvay, Arne  
; APPLICANT: Eriander, Mark G  
; APPLICANT: Glass, Charles A  
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor  
; TITLE OF INVENTION: VR3  
; FILE REFERENCE: Human VR3 receptors  
; CURRENT APPLICATION NUMBER: US/09/500,123  
; CURRENT FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-500-123-9

Query Match 51.6%; Score 383; DB 4; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPPAGGEVAELPGDESGTPGGAFLPSLIANLFBGSDGSLSPADASRPAGP 60  
DB 1 MADSSGPPAGGEVAELPGDESGTPGGAFLPSLIANLFBGSDGSLSPADASRPAGP 60  
QY 61 GGRPLRMKPGGARPKGVNPIIDLESTLYESSVVPGRKAPMDSLPGYGYRRHSSDN 120  
DB 61 GGRPLRMKPGGARPKGVNPIIDLESTLYESSVVPGRKAPMDSLPGYGYRRHSSDN 120  
QY 121 KMRKKIIEKQSPAPAPOPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180  
DB 121 KMRKKIIEKQSPAPAPOPPPILKVNRPILFDIVSRGSTADIDGLLPILLTHKKRL 180

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QY 181 TDEERESTGTCTCPKALINLSGRNDTIPVLIDIAERTGNMREFFINSPPEDITYRGQT 240
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Db 181 TDEERESTGTCTCPKALINLSGRNDTIPVLIDIAERTGNMREFFINSPPEDITYRGQT 240
QY 241 ALHIAIERCKHGYVELVAOGADVHAQARGFPOPKDEGYYFYFGEPLSLIACTNOPIH 300
;
Db 241 ALHIAIERCKHGYVELVAOGADVHAQARGFPOPKDEGYYFYFGEPLSLIACTNOPIH 300
QY 301 VNYLTENPHKXADMRQDSRGNTVLAHALVAIADNTRENTKTYKMYDILLKCARLFPDS 360
;
Db 301 VNYLTENPHKXADMRQDSRGNTVLAHALVAIADNTRENTKTYKMYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTGKI 383
;
Db 361 NLEAVLNNDGSLPLMAAKTGKI 383

RESULT 4
US-09-667-422-5
; Sequence 5, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; EARLIER FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (434)..(455)
; OTHER INFORMATION: TWI
; NAME/KEY: TRANSMEM
; LOCATION: (480)..(495)
; OTHER INFORMATION: TW2
US-09-667-422-5

Query Match
Best Local Similarity 2.2%; Score 16; DB 4; Length 511;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLIACTNO 297
;
Db 246 FYFGEPLSLIACTNO 261

RESULT 5
US-09-235-451-2
; Sequence 2, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 838
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; TYPE: PRT
; ORGANISM: R. rattus
US-09-235-451-2

Query Match
Best Local Similarity 2.2%; Score 16; DB 3; Length 838;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLIACTNO 297
;
Db 245 FYFGEPLSLIACTNO 260

RESULT 6
US-09-132-316-3
; Sequence 3, Application US/09132316B
; Patent No. 644440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488,110000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-132-316-3

Query Match
Best Local Similarity 2.2%; Score 16; DB 4; Length 838;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGEPLSLIACTNO 297
;
Db 245 FYFGEPLSLIACTNO 260

RESULT 7
US-09-667-422-9
; Sequence 9, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus sp.
; PUBLICATION INFORMATION:
; AUTHORS: Caterina, Michael J.
; AUTHORS: Schumacher, Mark A.
; AUTHORS: Tomlinaga, Makoto
; AUTHORS: Rosen, Tobias A.
; TITLE: The capsaicin receptor: a heat-activated ion channel in
; TITLE: the pain pathway
; JOURNAL: Nature
; VOLUME: 389
; PAGES: 816-824
; DATE: 1997
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US-09-667-422-9

Query Match 2.2% Score 16; DB 4; Length 838;  
Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLACTNQ 297  
DB 245 FYFGELPLSLACTNQ 260

RESULT 8

US-09-978-303-2  
Sequence 2, Application US/09978303  
Patent No. 6790629  
GENERAL INFORMATION:  
APPLICANT: Julius, David J.  
APPLICANT: Caterina, Michael J.  
TITLE OF INVENTION: Nucleic acid sequences encoding  
TITLE OF INVENTION: capsacin receptor and capsacin receptor-related  
FILE REFERENCE: UCAL084CON  
CURRENT APPLICATION NUMBER: US/09/978,303  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/235,451  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 60/072,151  
PRIOR FILING DATE: 1998-01-22  
PRIOR APPLICATION NUMBER: 08/915,461  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 838  
TYPE: PRT  
ORGANISM: R. rattus  
US-09-978-303-2

Query Match 2.2% Score 16; DB 4; Length 838;  
Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLACTNQ 297  
DB 245 FYFGELPLSLACTNQ 260

RESULT 9

US-09-197-636-2  
Sequence 2, Application US/09197636  
Patent No. 6239267  
GENERAL INFORMATION:  
APPLICANT: DUCKWORTH, DAVID  
APPLICANT: HAYES, PHILIP  
APPLICANT: MEADOWS, HELEN  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: US  
ZIP: 19482-0980  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,636

FILING DATE: 23-NOV-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UK 9805137.8

FILING DATE: 12-MAR-1998

APPLICATION NUMBER: UK 9815791.0

FILING DATE: 21-JUL-1998

APPLICATION NUMBER: UK 9819278.4

FILING DATE: 03-SEP-1998

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GP-30075

TELECOMMUNICATION INFORMATION:

TELEPHONE: 601-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 839 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-197-636-2  
Query Match 2.2% Score 16; DB 3; Length 839;  
Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLACTNQ 297  
DB 246 FYFGELPLSLACTNQ 261

RESULT 10

US-09-197-636-4  
Sequence 4, Application US/09197636  
Patent No. 6239267  
GENERAL INFORMATION:  
APPLICANT: DUCKWORTH, DAVID  
APPLICANT: HAYES, PHILIP  
APPLICANT: MEADOWS, HELEN  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: US  
ZIP: 19482-0980  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,636  
FILING DATE: 23-NOV-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 9805137.8  
FILING DATE: 12-MAR-1998  
APPLICATION NUMBER: UK 9815791.0  
FILING DATE: 21-JUL-1998  
APPLICATION NUMBER: UK 9819278.4  
FILING DATE: 03-SEP-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GP-30075



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 601-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 839 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-197-636-4

Query Match 2.2%; Score 16; DB 3; Length 839;  
Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297  
Db 246 FYFGELPLSLAQTQ 261

RESULT 11  
US-09-197-636-8  
Sequence 8, Application US/09197636  
Patent No. 6239267  
GENERAL INFORMATION:  
APPLICANT: DUCKWORTH, DAVID  
APPLICANT: HAYES, PHILIP  
APPLICANT: MEADOWS, HELEN  
APPLICANT: DAVIS, JOHN  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: US  
ZIP: 19482-0980  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,636  
FILING DATE: 23-NOV-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 9805137.8  
FILING DATE: 12-MAR-1998  
APPLICATION NUMBER: UK 9815791.0  
FILING DATE: 21-JUL-1998  
APPLICATION NUMBER: UK 9819278.4  
FILING DATE: 03-SEP-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GP-30075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 601-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 839 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-197-636-8

Query Match 2.2%; Score 16; DB 3; Length 839;  
Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297  
Db 246 FYFGELPLSLAQTQ 261

RESULT 12  
US-09-235-451-34  
Sequence 34, Application US/09235451  
GENERAL INFORMATION:  
APPLICANT: Julius, David J.  
APPLICANT: Caterina, Michael J.  
APPLICANT: Brake, Anthony J.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
FILE REFERENCE: 9076/084CIP  
CURRENT APPLICATION NUMBER: US/09/235,451  
CURRENT FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 60/072,151  
PRIOR FILING DATE: 1998-01-22  
PRIOR APPLICATION NUMBER: 08/915,461  
PRIOR FILING DATE: 1997-08-20  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 34  
LENGTH: 839  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-235-451-34

Query Match 2.2%; Score 16; DB 3; Length 839;  
Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297  
Db 246 FYFGELPLSLAQTQ 261

RESULT 13  
US-09-533-220A-2  
Sequence 2, Application US/09533220A  
Patent No. 6406908  
GENERAL INFORMATION:  
APPLICANT: McIntyre, Peter  
APPLICANT: James, Iain Fraser  
TITLE OF INVENTION: Human Vanilloid Receptor  
FILE REFERENCE: 4-30875A  
CURRENT APPLICATION NUMBER: US/09/533,220A  
CURRENT FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1  
PRIOR FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 1.30  
SEQ ID NO 2  
LENGTH: 839  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-533-220A-2

Query Match 2.2%; Score 16; DB 4; Length 839;  
Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 FYFGELPLSLAQTQ 297  
Db 246 FYFGELPLSLAQTQ 261

## RESULT 14

US-09-667-422-4

; Sequence 4, Application US/09667422

; Patent No. 6482611

; GENERAL INFORMATION:

; APPLICANT: Cortright, Daniel

; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof

; FILE REFERENCE: HCR

; CURRENT APPLICATION NUMBER: US/09/667,422

; CURRENT FILING DATE: 2001-06-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 4

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: TRANSMEM

; LOCATION: (434)..(455)

; OTHER INFORMATION: TM1

; NAME/KEY: TRANSMEM

; LOCATION: (480)..(495)

; OTHER INFORMATION: TM2

; NAME/KEY: TRANSMEM

; LOCATION: (510)..(530)

; OTHER INFORMATION: TM3

; NAME/KEY: TRANSMEM

; LOCATION: (543)..(569)

; OTHER INFORMATION: TM4

; NAME/KEY: TRANSMEM

; LOCATION: (577)..(596)

; OTHER INFORMATION: TMS

; NAME/KEY: TRANSMEM

; LOCATION: (656)..(684)

; OTHER INFORMATION: TM6

; US-09-667-422-4

Query Match 2.2%; Score 16; DB 4; Length 839;

Best Local Similarity 100.0%; Pred. No. 4.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLAQTNO 297

Db 246 FYFGELPLSLAQTNO 261

## RESULT 15

US-09-978-303-34

; Sequence 34, Application US/09978303

; Patent No. 6790629

; GENERAL INFORMATION:

; APPLICANT: Julius, David J.

; APPLICANT: Caterina, Michael J.

; APPLICANT: Brake, Anthony J.

; TITLE OF INVENTION: Nucleic acid sequences encoding

; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related

; FILE REFERENCE: UCA1084CON

; CURRENT APPLICATION NUMBER: US/09/978,303

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/235,451

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: 60/072,151

; PRIOR FILING DATE: 1998-01-22

; PRIOR APPLICATION NUMBER: 08/915,461

; PRIOR FILING DATE: 1997-08-20

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 34

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-303-34

Query Match 2.2%; Score 16; DB 4; Length 839;

Best Local Similarity 100.0%; Pred. No. 4.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 FYFGELPLSLAQTNO 297

Db 246 FYFGELPLSLAQTNO 261

Search completed: December 2, 2004, 22:55:04  
JOD time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 22:45:47 ; Search time 147 Seconds  
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Title: US-10-090-215-12

Perfect score: 742

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16: /cgn2\_6/ptodata/1/pubppa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubppa/US10D\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742	100.0	742	14	US-10-090-215-12 Sequence 12, Appl
2	736	99.2	831	15	US-10-342-844-76 Sequence 76, Appl
3	736	99.2	870	16	US-10-761-065-2 Sequence 2, Appl
4	736	99.2	871	10	US-09-870-090-2 Sequence 2, Appl
5	736	99.2	871	14	US-10-000-823-7 Sequence 7, Appl
6	736	99.2	871	14	US-10-171-319-17 Sequence 17, Appl
7	736	99.2	871	15	US-10-342-844-54 Sequence 54, Appl
8	736	99.2	871	15	US-10-342-844-58 Sequence 58, Appl
9	736	99.2	871	15	US-10-342-844-78 Sequence 78, Appl
10	736	99.2	871	17	US-10-415-570A-2 Sequence 2, Appl
11	668	90.0	803	15	US-10-342-844-56 Sequence 56, Appl
12	635	85.6	871	14	US-10-027-828-2 Sequence 2, Appl
13	635	85.6	871	14	US-10-027-828-4 Sequence 4, Appl

14	635	85.6	871	14	US-10-090-215-7 Sequence 7, Appl
15	635	85.6	871	15	US-10-342-844-60 Sequence 60, Appl
16	567	76.4	792	9	US-09-764-367A-2 Sequence 2, Appl
17	504	67.9	963	10	US-09-932-165-1477 Sequence 1477, Ap
18	452	60.9	602	10	US-09-870-090-4 Sequence 4, Appl
19	452	60.9	602	16	US-10-761-065-4 Sequence 4, Appl
20	449	60.5	625	10	US-09-932-165-1507 Sequence 1507, Ap
21	396	53.4	871	14	US-10-227-855A-3 Sequence 3, Appl
22	383	51.6	811	14	US-10-090-215-9 Sequence 9, Appl
23	365	49.2	803	9	US-09-764-367A-8 Sequence 8, Appl
24	362	48.8	559	14	US-10-297-022-10 Sequence 10, Appl
25	316	42.6	743	9	US-09-764-367A-11 Sequence 11, Appl
26	292	39.4	734	9	US-09-764-367A-11 Sequence 11, Appl
27	222	29.9	625	10	US-09-932-165-1506 Sequence 1506, Ap
28	202	27.2	498	14	US-10-168-651-2 Sequence 2, Appl
29	181	24.4	830	14	US-10-027-828-6 Sequence 6, Appl
30	181	24.4	871	14	US-10-027-828-8 Sequence 8, Appl
31	181	24.4	871	14	US-10-027-828-9 Sequence 9, Appl
32	181	24.4	871	14	US-10-027-828-10 Sequence 10, Appl
33	181	24.4	871	14	US-10-027-828-11 Sequence 11, Appl
34	181	24.4	871	14	US-10-342-844-66 Sequence 66, Appl
35	163	22.0	166	15	US-10-276-074-1571 Sequence 1571, Ap
36	112	15.1	803	15	US-10-342-844-62 Sequence 62, Appl
37	112	15.1	870	14	US-10-027-828-13 Sequence 13, Appl
38	112	15.1	871	14	US-10-227-855A-1 Sequence 1, Appl
39	112	15.1	871	14	US-10-171-319-14 Sequence 14, Appl
40	112	15.1	871	15	US-10-342-844-80 Sequence 80, Appl
41	112	15.1	871	15	US-10-342-844-84 Sequence 84, Appl
42	112	15.1	873	15	US-10-342-844-64 Sequence 64, Appl
43	87	11.7	420	14	US-10-027-828-7 Sequence 7, Appl
44	87	11.7	461	14	US-10-027-828-5 Sequence 5, Appl
45	68	9.2	852	14	US-10-027-828-15 Sequence 15, Appl

# ALIGNMENTS

RESULT 1

US-10-090-215-12

Sequence 12, Application US/10090215

Publication No. US20030032097A1

GENERAL INFORMATION:

APPLICANT: Dubin, Adrienne B

APPLICANT: Huvar, Arne

APPLICANT: Erlander, Mark G

APPLICANT: Glass, Charles A

TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor

FILE REFERENCE: Human VR3 receptors

CURRENT APPLICATION NUMBER: US/10/090,215

CURRENT FILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12

LENGTH: 742

TYPE: PRT

ORGANISM: Homo sapiens

US-10-090-215-12

Query Match	100.0%	Score 742;	DB 14;	Length 742;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 742;	Conservative 0;	Mismatches 0;	Gaps 0;	
QY	1	MADSSGPRAGPGVAVLPGDESGTGGGAAPLISLANTFEGDGSISPPADSRPAGP	60	
DB	1	MADSSGPRAGPGVAVLPGDESGTGGGAAPLISLANTFEGDGSISPPADSRPAGP	60	
QY	61	GDGPRNRMKFOGAFRGVPPIDILESTYESSVVGPKKAPMDSLFDYGYTHHSSDN	120	
DB	61	GDGPRNRMKFOGAFRGVPPIDILESTYESSVVGPKKAPMDSLFDYGYTHHSSDN	120	
QY	121	KRAKKTIIEQPOSQKAPAPPPILKVFNRPIFDIVSRGSTDLDGLLPLTLTKKRL	180	

Db	121	KRRKKKIIIEKQPSPRAPAPQPPPLIKVFNRRILFDIYSRGSSTADLDGILLPFLTHKKRL	180
Qy	181	TDEEFPBEPSTGTCLEPKALLANSGRNDTIPVLIDIAERTGMRPEFINSPPRDIYYRGOT	240
Db	181	TDEEFPBEPSTGTCLEPKALLANSGRNDTIPVLIDIAERTGMRPEFINSPPRDIYYRGOT	240
Qy	241	ALHAIATERKCHVVELLVIAQAGADVHAQAGREFPQCKDEGAFYFEGELPLSLAACTNOPHI	300
Db	241	ALHAIATERKCHVVELLVIAQAGADVHAQAGREFPQCKDEGAFYFEGELPLSLAACTNOPHI	300
Qy	301	VNYLTENPHKKADMRRODSRGNTVLHALVALADNTRENTKFTYMYDILLIKCARLPDS	360
Db	301	VNYLTENPHKKADMRRODSRGNTVLHALVALADNTRENTKFTYMYDILLIKCARLPDS	360
Qy	361	NLEAVLNNDGLSPILMAAATGKIGIFQHIIRREVTEDTBRHLSRFKDMAYGPYSSLYD	420
Db	361	NLEAVLNNDGLSPILMAAATGKIGIFQHIIRREVTEDTBRHLSRFKDMAYGPYSSLYD	420
Qy	421	LSLSLDTCGEEASVLEILVYNSKIEKNHEMLAVEPINELLRDKMRKFGASFYINVSYL	480
Db	421	LSLSLDTCGEEASVLEILVYNSKIEKNHEMLAVEPINELLRDKMRKFGASFYINVSYL	480
Qy	481	AMVIFLTLAYOGLBCTPPRYRTVDYRLAGEVITLFTGVLPFTNIXDLPHKKQPGV	540
Db	481	AMVIFLTLAYOGLBCTPPRYRTVDYRLAGEVITLFTGVLPFTNIXDLPHKKQPGV	540
Qy	541	NSLFIQGSFOLLFTIYSVVIYSAALYLAGIEBAYLAVWVFLVGMNNALETGKLITG	600
Db	541	NSLFIQGSFOLLFTIYSVVIYSAALYLAGIEBAYLAVWVFLVGMNNALETGKLITG	600
Qy	601	TSYIMIOKILFKOLFEPFLVYLLPMGVASVSLNRCAMNKCNEQNTCTPYTPSC	660
Db	601	TSYIMIOKILFKOLFEPFLVYLLPMGVASVSLNRCAMNKCNEQNTCTPYTPSC	660
Qy	661	RDESETFSTFLDLFKXITLGMGDLEMLSTKYPVFVILLVYIILLTFVLLNMLIALMGE	720
Db	661	RDESETFSTFLDLFKXITLGMGDLEMLSTKYPVFVILLVYIILLTFVLLNMLIALMGE	720
Qy	721	TVGQVSKESKHIMKLOSRRRL	742
Db	721	TVGQVSKESKHIMKLOSRRRL	742
RESULT 2			
US-10-342-844-76			
Sequence 76, Application US/10342844			
Publication No. US2004000937A1			
GENERAL INFORMATION:			
APPLICANT: Roos, Jack			
APPLICANT: Strandeman, Kenneth			
APPLICANT: VelicicLebi, G"n J			
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING			
TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM			
FILE REFERENCE: 37481-3307			
CURRENT APPLICATION NUMBER: US/10/342,844			
CURRENT FILING DATE: 2003-01-13			
PRIOR APPLICATION NUMBER: US 60/347,459			
PRIOR FILING DATE: 2002-01-11			
PRIOR APPLICATION NUMBER: US 60/401,171			
PRIOR FILING DATE: 2002-08-02			
PRIOR APPLICATION NUMBER: US 60/405,678			
PRIOR FILING DATE: 2002-08-20			
NUMBER OF SEQ ID NOS: 115			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 76			
LENGTH: 831			
TYPE: PRT			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: VARIANT			
LOCATION: 804, 816			
OTHER INFORMATION: Xaa = Any Amino Acid			
PUBLICATION INFORMATION:			

Query Match	99.2%	Score 736	DB 15	Length 831
Best Local Similarity	100.0%	Pred. No. 0		
Matches 736	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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DATABASE ENTRY DATE: 2001-10-16				
QY	1	MADSSRGGRAGPGEVAAKLPDSESGCPGGEAPFLSSIANLFEAGDGLSPSPDASRPAG	60	
DB	1	MADSSRGGRAGPGEVAAKLPDSESGCPGGEAPFLSSIANLFEAGDGLSPSPDASRPAG	60	
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DB	61	GDGRPNLMMKFGAERKGVNPEIDLESTLYESSVVGPKKAPMDSLFDYGYRRHSSDN	120	
QY	121	KRMKKIIIEKQPOSGKAPAPQPPILKAPNREILFDIVRSGSTADLDGLPLFLTHKKDL	180	
DB	121	KRMKKIIIEKQPOSGKAPAPQPPILKAPNREILFDIVRSGSTADLDGLPLFLTHKKDL	180	
QY	181	TDEERFEPSTGKTCLPKALNLSNGRNDTTPVLDIAERTGNMREPINSPFDDIYRGQT	240	
DB	181	TDEERFEPSTGKTCLPKALNLSNGRNDTTPVLDIAERTGNMREPINSPFDDIYRGQT	240	
QY	241	ALHAIIEKRCNHYVELLYAOGADVAOARGRFQPKDEGGYTFYFGLPFLSLAATNQHPI	300	
DB	241	ALHAIIEKRCNHYVELLYAOGADVAOARGRFQPKDEGGYTFYFGLPFLSLAATNQHPI	300	
QY	301	VNYLTENPHKKADMRQDSRGNTVLAHALVADNTRRENTKFTYKMYDLILLKCARLFPDS	360	
DB	301	VNYLTENPHKKADMRQDSRGNTVLAHALVADNTRRENTKFTYKMYDLILLKCARLFPDS	360	
QY	361	NLEAVLNNDGLSPILMMAAKTGKIGFQHTIRREVTDEDTREHLSRKRYDMAVGEVYSSLYD	420	
DB	361	NLEAVLNNDGLSPILMMAAKTGKIGFQHTIRREVTDEDTREHLSRKRYDMAVGEVYSSLYD	420	
QY	421	LSSLDTCGEBSVLEILVYNSKIENRHEMLAVEPINELLRDKMRKGAVSFYINVSYLEC	480	
DB	421	LSSLDTCGEBSVLEILVYNSKIENRHEMLAVEPINELLRDKMRKGAVSFYINVSYLEC	480	
QY	481	AMVIFETLLAYVQPLEGTEPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFPMKCEPV	540	
DB	481	AMVIFETLLAYVQPLEGTEPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFPMKCEPV	540	
QY	541	NSLFLDGSFOLLRYFYSLVLYVSALYLAGIAYLAVMFALVGMNNALYFPRGLKLTG	600	
DB	541	NSLFLDGSFOLLRYFYSLVLYVSALYLAGIAYLAVMFALVGMNNALYFPRGLKLTG	600	
QY	601	YSIMIQKILFKDLFRFLVLYLLFMIGVASALVSLNPCANMKVCNEDQNTCTVPTPSC	660	
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QY	661	RDSEFTSFLLDLFKLITGMGLEMLSSKRYVVPFILLVYTIILFVYLLNMLIALMGE	720	
DB	661	RDSEFTSFLLDLFKLITGMGLEMLSSKRYVVPFILLVYTIILFVYLLNMLIALMGE	720	
QY	721	TVGVYSKESKHIWKLO 736		
DB	721	TVGVYSKESKHIWKLO 736		
RESULT 3				
US-10-761-065-2				
Sequence 2, Application US//10761065				
Publication No. US20040137573A1				
GENERAL INFORMATION:				
APPLICANT: Pfizer, Inc.				
APPLICANT: Katsuhiko Shinjo				
APPLICANT: Hikaru Yabuuchi				
TITLE OF INVENTION: Human Vanilloid Receptor-like Proteins				
FILE REFERENCE: PC9979ADAM				
CURRENT APPLICATION NUMBER: US/10/761, 065				
CURRENT FILING DATE: 2004-01-20				

;; PRIOR APPLICATION NUMBER: US/09/870,090A  
;; PRIOR FILING DATE: 2001-05-30  
;; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins  
;; FILE REFERENCE: PC979A  
;; CURRENT APPLICATION NUMBER: US/09/870,090  
;; PRIOR APPLICATION NUMBER: US 60/208,156  
;; PRIOR FILING DATE: 2000-05-31  
;; NUMBER OF SEQ ID NOS: 9  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2  
;; LENGTH: 870  
;; TYPE: PRT  
;; ORGANISM: Human  
US-10-761-065-2

Query Match 99.2%; Score 736; DB 16; Length 870;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADSSGPRAGPGEVAELPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADASRPAGP 60
QY 61 GDGPRNLKMFQGAFRKGVNPIDLESTLYESSVVPKKAAMDLSFDYGYRRHSSDN 120
DB 61 GDGPRNLKMFQGAFRKGVNPIDLESTLYESSVVPKKAAMDLSFDYGYRRHSSDN 120
QY 121 KRWKRIIEKOPQSPKAPAPPPPLIKVFNRPILFDIYRSSTADLDGLPELTHKKRL 180
DB 121 KRWKRIIEKOPQSPKAPAPPPPLIKVFNRPILFDIYRSSTADLDGLPELTHKKRL 180
QY 181 TDEFRERSTGKTCLPKALNLSNGRNDTIVLDIAERTGNMREFINSPPFDIYYRGOT 240
DB 181 TDEFRERSTGKTCLPKALNLSNGRNDTIVLDIAERTGNMREFINSPPFDIYYRGOT 240
QY 241 ALHIAIERCHYVELVAQADVAHAQARGFPQKDEGQYFYFGEPLSLAAGTNOPIHI 300
DB 241 ALHIAIERCHYVELVAQADVAHAQARGFPQKDEGQYFYFGEPLSLAAGTNOPIHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXKDMAGPVYSSLYD 420
DB 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXKDMAGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYLEC 480
QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLEFFTNIKDLFMKCPGV 540
DB 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLEFFTNIKDLFMKCPGV 540
QY 541 NSLIFDGSFQLLYFYISVLAIVSALYLAGIEAYLAVVAFVLVGMNNAALYFTRGLKLTG 600
DB 541 NSLIFDGSFQLLYFYISVLAIVSALYLAGIEAYLAVVAFVLVGMNNAALYFTRGLKLTG 600
QY 601 TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC 660
DB 601 TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC 660
QY 661 RDSEFTSTFLDLDFKLITGMGDLMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
DB 661 RDSEFTSTFLDLDFKLITGMGDLMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
QY 721 TVGVSKESKHIWKQ 736
DB 721 TVGVSKESKHIWKQ 736
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RESULT 4  
US-09-870-090-2  
; Sequence 2, Application US/09870090  
; Publication No. US20030017527A1

;; GENERAL INFORMATION:  
;; APPLICANT: Pfizer Product Inc.  
;; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins  
;; FILE REFERENCE: PC979A  
;; CURRENT APPLICATION NUMBER: US/09/870,090  
;; PRIOR APPLICATION NUMBER: US 60/208,156  
;; PRIOR FILING DATE: 2000-05-31  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 2  
;; LENGTH: 871  
;; TYPE: PRT  
;; ORGANISM: Human  
US-09-870-090-2

Query Match 99.2%; Score 736; DB 10; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADSSGPRAGPGEVAELPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADASRPAGP 60
DB 1 MADSSGPRAGPGEVAELPGDESGTPGGEAPPLSLANLFGEDGSLSPSPADASRPAGP 60
QY 61 GDGPRNLKMFQGAFRKGVNPIDLESTLYESSVVPKKAAMDLSFDYGYRRHSSDN 120
DB 61 GDGPRNLKMFQGAFRKGVNPIDLESTLYESSVVPKKAAMDLSFDYGYRRHSSDN 120
QY 121 KRWKRIIEKOPQSPKAPAPPPPLIKVFNRPILFDIYRSSTADLDGLPELTHKKRL 180
DB 121 KRWKRIIEKOPQSPKAPAPPPPLIKVFNRPILFDIYRSSTADLDGLPELTHKKRL 180
QY 181 TDEFRERSTGKTCLPKALNLSNGRNDTIVLDIAERTGNMREFINSPPFDIYYRGOT 240
DB 181 TDEFRERSTGKTCLPKALNLSNGRNDTIVLDIAERTGNMREFINSPPFDIYYRGOT 240
QY 241 ALHIAIERCHYVELVAQADVAHAQARGFPQKDEGQYFYFGEPLSLAAGTNOPIHI 300
DB 241 ALHIAIERCHYVELVAQADVAHAQARGFPQKDEGQYFYFGEPLSLAAGTNOPIHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHVAIADNRENTKFTVKNYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXKDMAGPVYSSLYD 420
DB 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDDETRHLSRFXKDMAGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKMRKFGAVSFYINVSYLEC 480
QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLEFFTNIKDLFMKCPGV 540
DB 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLEFFTNIKDLFMKCPGV 540
QY 541 NSLIFDGSFQLLYFYISVLAIVSALYLAGIEAYLAVVAFVLVGMNNAALYFTRGLKLTG 600
DB 541 NSLIFDGSFQLLYFYISVLAIVSALYLAGIEAYLAVVAFVLVGMNNAALYFTRGLKLTG 600
QY 601 TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC 660
DB 601 TYSIMIQKILFKDLFRFLVYLLEFMIGYASALVSLNLCANMKVCNEQDQNTCTVPTPSC 660
QY 661 RDSEFTSTFLDLDFKLITGMGDLMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
DB 661 RDSEFTSTFLDLDFKLITGMGDLMLSTKYPVVFIIILVTYIIILTFVLLNMLTALMGE 720
QY 721 TVGVSKESKHIWKQ 736
DB 721 TVGVSKESKHIWKQ 736
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RESULT 5  
US-10-000-823-7  
; Sequence 7, Application US/10000823  
; Publication No. US20030027164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NO  
; FILE REFERENCE: DOI109NP  
; CURRENT APPLICATION NUMBER: US/10/000,823  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/250,587  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 871  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-000-823-7

Query Match 99.2%; Score 736; DB 14; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSLANLFEDEGSLSPSPADASRPAGP 60  
DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSLANLFEDEGSLSPSPADASRPAGP 60  
QY 61 GGRPNLMMKFGARPKGVNPIDILESTLYESSVVPQKAPMDSLPDYGYRRHSSDN 120  
DB 61 GGRPNLMMKFGARPKGVNPIDILESTLYESSVVPQKAPMDSLPDYGYRRHSSDN 120  
QY 121 KWRKRIIEKOPQSKAPAPOPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180  
DB 121 KWRKRIIEKOPQSKAPAPOPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180  
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DB 121 KWRKRIIEKOPQSKAPAPOPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180  
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QY 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQDEGGYVFGELPLSLAACTNQHPI 300  
DB 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQDEGGYVFGELPLSLAACTNQHPI 300  
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRNTKFTYKAYDILLKCARLFPDS 360  
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRNTKFTYKAYDILLKCARLFPDS 360  
QY 361 NIEAVLANDGSLPLMAAATGKIGIFOHIIIRREVDEDTRHLSRKFQMAVGPVYSSLYD 420  
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QY 421 LSSLTQCEBAVLEILVYNSKIENRHEMLAVEPINELLRDKMRKGAVSFTIYVSYLC 480  
DB 421 LSSLTQCEBAVLEILVYNSKIENRHEMLAVEPINELLRDKMRKGAVSFTIYVSYLC 480  
QY 481 AMVIFTLAAYOPLGTEPPYPRYRTVDYLRLAGEVITLFTGVLPFTYINIKOLFMMKCGV 540  
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QY 541 NSLFLDGSFQQLYFYISVLYVSAAIYLAGIAYAVWVFALVGMNALLYTRGLKLTG 600  
DB 541 NSLFLDGSFQQLYFYISVLYVSAAIYLAGIAYAVWVFALVGMNALLYTRGLKLTG 600  
QY 601 TYSIMQIKLFPDLRPLLVYLLFMIGYASALVSLNPNANKVCEBDQTCVFTYSSC 660  
DB 601 TYSIMQIKLFPDLRPLLVYLLFMIGYASALVSLNPNANKVCEBDQTCVFTYSSC 660  
QY 661 RDESEFSTFLDLFLKLTIGMGDLEMLSTKYVEVEIILLVYIILTFVLLNMLTALNGE 720  
DB 661 RDESEFSTFLDLFLKLTIGMGDLEMLSTKYVEVEIILLVYIILTFVLLNMLTALNGE 720

QY 721 TVGQVSKSKHIMKIQ 736  
DB 721 TVGQVSKSKHIMKIQ 736

RESULT 6  
US-10-171-319-17  
; Sequence 17, Application US/1017319  
; Publication No. US20030157633A1  
; GENERAL INFORMATION:  
; APPLICANT: Arden Patapoutian  
; APPLICANT: Andrea Peler  
; APPLICANT: Peter McIntyre  
; APPLICANT: Stuart Bevan  
; APPLICANT: Chuanzheng Song  
; APPLICANT: Pamosh Ganju  
; TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS  
; FILE REFERENCE: 4-32048A  
; CURRENT APPLICATION NUMBER: US/10/171,319  
; PRIOR FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 60/297,835  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/351,238  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/352,914  
; PRIOR FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: 60/357,161  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/381,086  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: 60/381,739  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FaetSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 871  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-171-319-17

Query Match 99.2%; Score 736; DB 14; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSLANLFEDEGSLSPSPADASRPAGP 60  
DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSLANLFEDEGSLSPSPADASRPAGP 60  
QY 61 GGRPNLMMKFGARPKGVNPIDILESTLYESSVVPQKAPMDSLPDYGYRRHSSDN 120  
DB 61 GGRPNLMMKFGARPKGVNPIDILESTLYESSVVPQKAPMDSLPDYGYRRHSSDN 120  
QY 121 KWRKRIIEKOPQSKAPAPOPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180  
DB 121 KWRKRIIEKOPQSKAPAPOPPLIKVFNRPILFDIYSRGSTADLDGLPLTHKKRL 180  
QY 181 TDEEFPSTGTCTCPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRQGT 240  
DB 181 TDEEFPSTGTCTCPKALNLSNGRNDTIPVLDIAERTGNMREFFINSPPFDIYRQGT 240  
QY 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQDEGGYVFGELPLSLAACTNQHPI 300  
DB 241 ALHIAIERCKHYVELVAQADVAHQAQGRFPQDEGGYVFGELPLSLAACTNQHPI 300  
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRNTKFTYKAYDILLKCARLFPDS 360  
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRNTKFTYKAYDILLKCARLFPDS 360  
QY 361 NIEAVLANDGSLPLMAAATGKIGIFOHIIIRREVDEDTRHLSRKFQMAVGPVYSSLYD 420  
DB 361 NIEAVLANDGSLPLMAAATGKIGIFOHIIIRREVDEDTRHLSRKFQMAVGPVYSSLYD 420

QY 421 LSLDTGCEBASVLEILVYNSKIENRHEMLAVEPINELLRDKRRKFGAVSFYINVSYLIC 480  
Db 421 LSLDTGCEBASVLEILVYNSKIENRHEMLAVEPINELLRDKRRKFGAVSFYINVSYLIC 480  
QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCCPGV 540  
Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCCPGV 540  
QY 541 NSLFTDGSFOLLYFYISVLYVSALYLAGIAYLAVWVFPALVGMNALYFTRGLKLTG 600  
Db 541 NSLFTDGSFOLLYFYISVLYVSALYLAGIAYLAVWVFPALVGMNALYFTRGLKLTG 600  
QY 601 TYSIMIQILFKDIFRFLVLYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660  
Db 601 TYSIMIQILFKDIFRFLVLYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660  
QY 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720  
Db 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720  
QY 721 TVGVSKSKHIMKIQ 736  
Db 721 TVGVSKSKHIMKIQ 736

## RESULT 7

US-10-342-844-54  
Sequence 54, Application US/10342844  
Publication No. US20040009537A1  
GENERAL INFORMATION:  
APPLICANT: Roos, Jack  
APPLICANT: Stauderman, Kenneth  
APPLICANT: Velicelcib, G'n.1  
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING  
FILE REFERENCE: 37481-3307  
CURRENT APPLICATION NUMBER: US/10/342, 844  
CURRENT FILING DATE: 2003-01-13  
PRIOR APPLICATION NUMBER: US 60/347,459  
PRIOR FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: US 60/401,171  
PRIOR FILING DATE: 2002-08-02  
PRIOR APPLICATION NUMBER: US 60/405,678  
PRIOR FILING DATE: 2002-08-20  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54  
LENGTH: 871  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: Genbank XP\_027181  
DATABASE ENTRY DATE: 2002-09-01  
US-10-342-844-54

Query Match 99.2%; Score 736; DB 15; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSSEPRAGPGFVALPDDESGTGGGAFFPLSLANTREGFGSLSPSPADSRAPG 60  
Db 1 MADSSSEPRAGPGFVALPDDESGTGGGAFFPLSLANTREGFGSLSPSPADSRAPG 60  
QY 61 GDRPNLRMFKFOGAFRGVNPIDILLESSTYESSVVGPKKAPWDSLFYGYVHHSSDN 120  
Db 61 GDRPNLRMFKFOGAFRGVNPIDILLESSTYESSVVGPKKAPWDSLFYGYVHHSSDN 120  
QY 121 KRRRKKTIERKOPSPKAPAPQPPPIIKVFNRPILFDIVSGSTADLDGLLPFLITHKRL 180  
Db 121 KRRRKKTIERKOPSPKAPAPQPPPIIKVFNRPILFDIVSGSTADLDGLLPFLITHKRL 180  
QY 181 TDEEFREPSTGKCTCPKALNLSGRNDTLPVLLDIERGNMREFINSPFDIYYRGOT 240  
Db 181 TDEEFREPSTGKCTCPKALNLSGRNDTLPVLLDIERGNMREFINSPFDIYYRGOT 240

Db 181 TDEEFREPSTGKCTCPKALNLSGRNDTLPVLLDIERGNMREFINSPFDIYYRGOT 240  
QY 241 ALHIAIERCHRYVELLVAOGADVYAOARGPPOPKDEGYFYEGELSLAACNPOHI 300  
Db 241 ALHIAIERCHRYVELLVAOGADVYAOARGPPOPKDEGYFYEGELSLAACNPOHI 300  
QY 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKVKYDILLKCARLPDS 360  
Db 301 VNYLTENPHKXADMRQDSRGNTVLAALVAIADNTRENTKVKYDILLKCARLPDS 360  
QY 361 NLEAVLNDGSLPLMAAKTKIGI FQHIIRREVTDETRHLSRKKOMAVGPVYSYD 420  
Db 361 NLEAVLNDGSLPLMAAKTKIGI FQHIIRREVTDETRHLSRKKOMAVGPVYSYD 420  
QY 421 LSLDTGCEBASVLEILVYNSKIENRHEMLAVEPINELLRDKRRKFGAVSFYINVSYLIC 480  
Db 421 LSLDTGCEBASVLEILVYNSKIENRHEMLAVEPINELLRDKRRKFGAVSFYINVSYLIC 480  
QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCCPGV 540  
Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTNIKDLFMKCCPGV 540  
QY 541 NSLFTDGSFOLLYFYISVLYVSALYLAGIAYLAVWVFPALVGMNALYFTRGLKLTG 600  
Db 541 NSLFTDGSFOLLYFYISVLYVSALYLAGIAYLAVWVFPALVGMNALYFTRGLKLTG 600  
QY 601 TYSIMIQILFKDIFRFLVLYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660  
Db 601 TYSIMIQILFKDIFRFLVLYLLFMIGYASALVSLNLCAMKVCNEQNTCTVPTPSC 660  
QY 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720  
Db 661 RDSEFTSTFLDLFLKLTIGMDLEMLSTKYPVVFIILVTYIILTFVLINMLIALMGE 720  
QY 721 TVGVSKSKHIMKIQ 736  
Db 721 TVGVSKSKHIMKIQ 736

## RESULT 8

US-10-342-844-58  
Sequence 58, Application US/10342844  
Publication No. US20040009537A1  
GENERAL INFORMATION:  
APPLICANT: Roos, Jack  
APPLICANT: Stauderman, Kenneth  
APPLICANT: Velicelcib, G'n.1  
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING  
FILE REFERENCE: 37481-3307  
CURRENT APPLICATION NUMBER: US/10/342, 844  
CURRENT FILING DATE: 2003-01-13  
PRIOR APPLICATION NUMBER: US 60/347,459  
PRIOR FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: US 60/401,171  
PRIOR FILING DATE: 2002-08-02  
PRIOR APPLICATION NUMBER: US 60/405,678  
PRIOR FILING DATE: 2002-08-20  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 58  
LENGTH: 871  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: Genbank BAB69040  
DATABASE ENTRY DATE: 2001-10-02  
US-10-342-844-58

Query Match 99.2%; Score 736; DB 15; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

QY 1 MADSSEGRAPGGEVAILPGDESGTGGGEAPPLSLANLFFGEGDGLSPSPADASRPAGP 60
DB 1 MADSSEGRAPGGEVAILPGDESGTGGGEAPPLSLANLFFGEGDGLSPSPADASRPAGP 60
QY 61 GDGRPNLMMKQGAARKKVNPIDLESTLYESSVVPQKAPMDSLFDTGYTHHSSDN 120
DB 61 GDGRPNLMMKQGAARKKVNPIDLESTLYESSVVPQKAPMDSLFDTGYTHHSSDN 120
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
QY 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
DB 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
QY 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
DB 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
QY 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
QY 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
QY 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
DB 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
QY 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
DB 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
QY 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
DB 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
QY 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
DB 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
QY 721 TVGQVSKESKHIMKQ 736
DB 721 TVGQVSKESKHIMKQ 736
QY 721 TVGQVSKESKHIMKQ 736
DB 721 TVGQVSKESKHIMKQ 736

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCSSION NUMBER: Genbank AAC16127
; DATABASE ENTRY DATE: 2000-09-26
; US-10-342-844-78

Query Match      99.2%; Score 736; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSEGRAPGGEVAILPGDESGTGGGEAPPLSLANLFFGEGDGLSPSPADASRPAGP 60
DB 1 MADSSEGRAPGGEVAILPGDESGTGGGEAPPLSLANLFFGEGDGLSPSPADASRPAGP 60
QY 61 GDGRPNLMMKQGAARKKVNPIDLESTLYESSVVPQKAPMDSLFDTGYTHHSSDN 120
DB 61 GDGRPNLMMKQGAARKKVNPIDLESTLYESSVVPQKAPMDSLFDTGYTHHSSDN 120
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
QY 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
DB 121 KMRKRIIEKQPOSEKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLPELTHKKRL 180
QY 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
DB 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
QY 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
DB 181 TDEEFREPGTGTCLPKALNLSNGRNDTIPYLLDIAERTGMREFINSPPFDIYYRQGT 240
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
QY 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
DB 241 ALHIAIERCKHYVELLVAOGADVAOARGRFPQKDGSGYFGEPLSLAAGTNOPIH 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLKCARLFPDS 360
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
QY 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
DB 361 NIEAVLNDGSLPLMAAKTGKIGIFOHIIIRREVDEDETRHLSRKFKOMAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKMRKFGAVSFYINVSYLEC 480
QY 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
QY 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
DB 481 AMVIFTLTAAYOPLBGTTPPYRTVDYLRLAGEVITLFTGVLPFTNIXDLFMKKCPGV 540
QY 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
DB 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
QY 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
DB 541 NSLFTDGSFOLLFTYSVLYVSALYLAGIEAYIAWVFAVLGMNMLYFTRGKLGTG 600
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
QY 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
DB 601 TYSIMOKLIFKDLRFLVYLLFMIGYASALVSLNPCANNKVCNEODTNCVTPYPSG 660
QY 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
DB 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
QY 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
DB 661 RDSEFTSTFLDLFKLTIGMDLEMLSTKYVPVFIILVYIILTFVLLNMLTALMGE 720
QY 721 TVGQVSKESKHIMKQ 736
DB 721 TVGQVSKESKHIMKQ 736
QY 721 TVGQVSKESKHIMKQ 736
DB 721 TVGQVSKESKHIMKQ 736

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RESULT 10
US-10-415-570A-2
; Sequence 2, Application US/10415570A
; Publication No. US20040198649A1
; GENERAL INFORMATION:
; APPLICANT: Davis, John Beresford

```

; APPLICANT: Gunthorpe, Martin James  
 ; APPLICANT: Egeon, Julie  
 ; APPLICANT: Smart, Darren  
 ; TITLE OF INVENTION: New Use  
 ; FILE REFERENCE: P32689  
 ; CURRENT APPLICATION NUMBER: US/10/415,570A  
 ; PRIOR FILING DATE: 2003-04-23  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/04739  
 ; PRIOR FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: GB 0026114.9  
 ; PRIOR FILING DATE: 2000-10-25  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-415-570A-2

Query Match 99.2%; Score 736; DB 17; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGRAGGRTAELPGDESGTGGHAPLSLALPFGEDGSLSPSPADARPPGP 60  
 DB 1 MADSEGRAGGRTAELPGDESGTGGHAPLSLALPFGEDGSLSPSPADARPPGP 60  
 QY 61 GDGRPNLMKFOGAFKGVNPIDLLSTLYESSVVPQPKAPMDSLFDYGYRHHSSDN 120  
 DB 61 GDGRPNLMKFOGAFKGVNPIDLLSTLYESSVVPQPKAPMDSLFDYGYRHHSSDN 120  
 QY 121 KRWKRIIEKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRL 180  
 DB 121 KRWKRIIEKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRL 180  
 QY 121 KRWKRIIEKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRL 180  
 DB 121 KRWKRIIEKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRL 180  
 QY 181 TDEERESTGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQT 240  
 DB 181 TDEERESTGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQT 240  
 QY 181 TDEERESTGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQT 240  
 DB 181 TDEERESTGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQT 240  
 QY 241 ALHAIERCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI 300  
 DB 241 ALHAIERCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI 300  
 QY 241 ALHAIERCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI 300  
 DB 241 ALHAIERCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI 300  
 QY 301 VNYLTENPKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDS 360  
 DB 301 VNYLTENPKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDS 360  
 QY 301 VNYLTENPKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDS 360  
 DB 301 VNYLTENPKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDS 360  
 QY 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYD 420  
 DB 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYD 420  
 QY 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYD 420  
 DB 361 NLEAVLNDGSLPLMAKTKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYD 420  
 QY 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480  
 DB 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480  
 QY 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480  
 DB 421 LSLDTGCEASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLIC 480  
 QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGV 540  
 DB 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGV 540  
 QY 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGV 540  
 DB 481 AMVIFTLTAYYQPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGV 540  
 QY 541 NSLITDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTG 600  
 DB 541 NSLITDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTG 600  
 QY 541 NSLITDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTG 600  
 DB 541 NSLITDGSFOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTG 600  
 QY 601 TYSIMIQKILFKDLFRFLVILFMIGYASALVSLINFCAMKVCNEDQCTVPTPSC 660  
 DB 601 TYSIMIQKILFKDLFRFLVILFMIGYASALVSLINFCAMKVCNEDQCTVPTPSC 660  
 QY 601 TYSIMIQKILFKDLFRFLVILFMIGYASALVSLINFCAMKVCNEDQCTVPTPSC 660  
 DB 601 TYSIMIQKILFKDLFRFLVILFMIGYASALVSLINFCAMKVCNEDQCTVPTPSC 660  
 QY 661 RDSSTFSTLLDLFLTLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLIALMGE 720  
 DB 661 RDSSTFSTLLDLFLTLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLIALMGE 720  
 QY 661 RDSSTFSTLLDLFLTLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLIALMGE 720  
 DB 661 RDSSTFSTLLDLFLTLTGMDLEMLSTKYPVVEIILVTVIILFTVLLNMLIALMGE 720  
 QY 721 TVGVSKESKHIWKLO 736  
 DB 721 TVGVSKESKHIWKLO 736

DB 721 TVGVSKESKHIWKLO 736

RESULT 11  
 ; US-10-342-844-56  
 ; Sequence 56, Application US/10342844  
 ; Publication No. US2004009537A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stauderman, Kenneth  
 ; APPLICANT: Roos, Jack  
 ; APPLICANT: Vellelebi, Cn'l  
 ; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING  
 ; FILE REFERENCE: 37481-3307  
 ; CURRENT APPLICATION NUMBER: US/10/342,844  
 ; PRIOR FILING DATE: 2003-01-13  
 ; PRIOR APPLICATION NUMBER: US 60/347,459  
 ; PRIOR FILING DATE: 2002-01-11  
 ; PRIOR APPLICATION NUMBER: US 60/401,171  
 ; PRIOR FILING DATE: 2002-08-02  
 ; PRIOR APPLICATION NUMBER: US 60/405,678  
 ; PRIOR FILING DATE: 2002-08-20  
 ; NUMBER OF SEQ ID NOS: 115  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 56  
 ; LENGTH: 803  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: Genbank AAK69487  
 ; DATABASE ENTRY DATE: 2001-07-02  
 US-10-342-844-56

Query Match 90.0%; Score 668; DB 15; Length 803;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFOAFKGVNPIDLLSTLYESSVVPQPKAPMDSLFDYGYRHHSSDNKRWKRII 128  
 DB 1 MKFOAFKGVNPIDLLSTLYESSVVPQPKAPMDSLFDYGYRHHSSDNKRWKRII 128  
 QY 129 EKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRLTDEEREP 188  
 DB 129 EKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRLTDEEREP 188  
 QY 129 EKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRLTDEEREP 188  
 DB 129 EKOPQSKAPAPPPILKVFENRILFDIVSRGSTADLDGLPFLTHKKRLTDEEREP 188  
 QY 189 STGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQTALHAIER 248  
 DB 189 STGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQTALHAIER 248  
 QY 189 STGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQTALHAIER 248  
 DB 189 STGTCLPKALNLSNGRNDTIPVLDIAERTGMREFINSPPRDYIRGQTALHAIER 248  
 QY 249 RCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI VNYLTENP 308  
 DB 249 RCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI VNYLTENP 308  
 QY 249 RCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI VNYLTENP 308  
 DB 249 RCKHYVELVAOQADVAOARGRFQPKDEGGYFGEPLPLSLAAGTNOHI VNYLTENP 308  
 QY 309 HKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDSNLFAVANN 368  
 DB 309 HKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDSNLFAVANN 368  
 QY 309 HKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDSNLFAVANN 368  
 DB 309 HKKADMRQDSRGNTVLAIAADNTRENTKFTYKXVDLLKCARLPDSNLFAVANN 368  
 QY 369 DGLSPIMMAAATGKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428  
 DB 369 DGLSPIMMAAATGKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428  
 QY 369 DGLSPIMMAAATGKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428  
 DB 369 DGLSPIMMAAATGKIGIFOHIIIRREVTDETRHLSRFXKMAAGPVYSSLYDLSLDTG 428  
 QY 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488  
 DB 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488  
 QY 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488  
 DB 429 EASVLEILVYNSKIENRHEMLAVEPINELDRKMRKFGAVSYINVSYLICAMVIFTLT 488  
 QY 489 AAYOPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGVNSLFDIGS 548  
 DB 489 AAYOPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGVNSLFDIGS 548  
 QY 489 AAYOPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGVNSLFDIGS 548  
 DB 489 AAYOPLEGTPPYRTVDYRLAGEVITLFTGVLFFFTNIKDLFMKCKGVNSLFDIGS 548  
 QY 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTGYSIMIQ 608  
 DB 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTGYSIMIQ 608  
 QY 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTGYSIMIQ 608  
 DB 549 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTGYSIMIQ 608  
 QY 481 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTGYSIMIQ 540  
 DB 481 FOLLFYISVLAIVSALYLAGIEAYLAVMVFAVLGMMNALFTTRGLKLTGYSIMIQ 540

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QY 609 ILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSCRDSETEST 668
DB 541 ILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSCRDSETEST 600
QY 669 FLDDFKLITIGMDLEMLSTKYVVFILLVYIIILTVLLNMLALMGSTVQVSKR 728
DB 601 FLDDFKLITIGMDLEMLSTKYVVFILLVYIIILTVLLNMLALMGSTVQVSKR 660
QY 729 SKHWKIQ 736
DB 661 SKHWKIQ 668

RESULT 12
US-10-027-828-2
; Sequence 2, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudepeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-027-828-2

Query Match      85.6%; Score 635; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGEVAVELPGDESGTGGRAFLPSSLANIFEGEDGSLSPADASRPAG 60
DB 1 MADSSGPRAGGEVAVELPGDESGTGGRAFLPSSLANIFEGEDGSLSPADASRPAG 60
QY 61 GGRPVLRMKFGAFAFKGVNPIDLESTLYESSVVPGRKAPMDSLFYGYTRHSSDN 120
DB 61 GGRPVLRMKFGAFAFKGVNPIDLESTLYESSVVPGRKAPMDSLFYGYTRHSSDN 120
QY 121 KRWKXKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADLDGLPFLTHKKKL 180
DB 121 KRWKXKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADLDGLPFLTHKKKL 180
QY 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
DB 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDDEGAFYFGSLPLSLAAGTQPHI 300
DB 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDDEGAFYFGSLPLSLAAGTQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTVMYDILLIKCARLPDPS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTVMYDILLIKCARLPDPS 360
QY 361 NLEAVANNGLSLMAAAKTGKIGIPIHIIIRREVTDDEPRHLSRKEDMAVGVYSGLVD 420
DB 361 NLEAVANNGLSLMAAAKTGKIGIPIHIIIRREVTDDEPRHLSRKEDMAVGVYSGLVD 420
QY 421 LSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLDKWRKGAVSFYINVSYL 480
DB 421 LSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLDKWRKGAVSFYINVSYL 480

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QY 481 ANVIFTLRAYYOPLEGTPPYRTTVDYIRLAGEVITLFTGLPFTNLIKLEMKKCGV 540
DB 481 ANVIFTLRAYYOPLEGTPPYRTTVDYIRLAGEVITLFTGLPFTNLIKLEMKKCGV 540
QY 541 NSLFDGSRQLLYFYISVLYISALYLAGIRAYLVAMVFAVLGMNANLYTRGKL 600
DB 541 NSLFDGSRQLLYFYISVLYISALYLAGIRAYLVAMVFAVLGMNANLYTRGKL 600
QY 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSC 660
DB 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEDQNTCTVPTPSC 660
QY 661 RDEFTSTFLDLFKLITIGMDLEMLSTKYVVFILLVYIIILTVLLNMLALMG 720
DB 661 RDEFTSTFLDLFKLITIGMDLEMLSTKYVVFILLVYIIILTVLLNMLALMG 720
QY 721 TVGVSKSKHWKIQ 736
DB 721 TVGVSKSKHWKIQ 736

RESULT 13
US-10-027-828-4
; Sequence 4, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudepeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 871
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-027-828-4

Query Match      85.6%; Score 635; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGEVAVELPGDESGTGGRAFLPSSLANIFEGEDGSLSPADASRPAG 60
DB 1 MADSSGPRAGGEVAVELPGDESGTGGRAFLPSSLANIFEGEDGSLSPADASRPAG 60
QY 61 GGRPVLRMKFGAFAFKGVNPIDLESTLYESSVVPGRKAPMDSLFYGYTRHSSDN 120
DB 61 GGRPVLRMKFGAFAFKGVNPIDLESTLYESSVVPGRKAPMDSLFYGYTRHSSDN 120
QY 121 KRWKXKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADLDGLPFLTHKKKL 180
DB 121 KRWKXKIIKQPSRPAPOPPIIKVFNRPILFDIVSRGSTADLDGLPFLTHKKKL 180
QY 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
DB 181 TDEEFREBPGTGTCLPKALINLSNGRNDTTPVLLDIAERTGNMREINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDDEGAFYFGSLPLSLAAGTQPHI 300
DB 241 ALHIAIERCKHYVELLVAGADVHAQARGFPQPDDEGAFYFGSLPLSLAAGTQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTVMYDILLIKCARLPDPS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTVMYDILLIKCARLPDPS 360

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Qy 361 NLEAVLNNDGSLPLMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAGPVYSSLYD 420
Db 361 NLEAVLNNDGSLPLMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAGPVYSSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYL 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYL 480
Qy 481 AMVIFTLTAAVYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Db 481 AMVIFTLTAAVYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Qy 541 NSLFDGSPOLLFYISVLYVSALYLAGIEAYLAVVFPALVGMNALYFTRGKLTG 600
Db 541 NSLFDGSPOLLFYISVLYVSALYLAGIEAYLAVVFPALVGMNALYFTRGKLTG 600
Qy 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLNPKANKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLNPKANKVCNEDQNTCTVPTPSC 660
Qy 661 RDSEFTSTFLDLFLTLTGMDLEMLSTKYPVVFIILVTYIILFTVLLNMLTALMGE 720
Db 661 RDSEFTSTFLDLFLTLTGMDLEMLSTKYPVVFIILVTYIILFTVLLNMLTALMGE 720
Qy 721 TVGVSKESKHIWKIQ 736
Db 721 TVGVSKESKHIWKIQ 736

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## RESULT 14

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US-10-090-215-7
; Sequence 7, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Huvart, Arne
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-7

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Query Match 85.6%; Score 635; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSLANLFGCEDGSLSPSPADASRPAGP 60
Db 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSLANLFGCEDGSLSPSPADASRPAGP 60
Qy 61 GDGPRNLPMKFOGAFRRKVPNPIDLESTLYESSVVPKAPMDSLDYGYTHHSSDN 120
Db 61 GDGPRNLPMKFOGAFRRKVPNPIDLESTLYESSVVPKAPMDSLDYGYTHHSSDN 120
Qy 121 KRWKKLIEKOPSPKAPAPQPPILKVFNPILFDIYSRGSTADLDGLPFLTHKKRL 180
Db 121 KRWKKLIEKOPSPKAPAPQPPILKVFNPILFDIYSRGSTADLDGLPFLTHKKRL 180
Qy 181 TDEFRPSTGCTCLPKALNLSNGRNDTIVLLDIARTGNMRPINSPPRIYYRCQT 240
Db 181 TDEFRPSTGCTCLPKALNLSNGRNDTIVLLDIARTGNMRPINSPPRIYYRCQT 240
Qy 241 ALHAIERCKHYVELLVAOGADVAOARGFPQPKDGGYFYRGEELPLSLAACNQH 300
Db 241 ALHAIERCKHYVELLVAOGADVAOARGFPQPKDGGYFYRGEELPLSLAACNQH 300

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Db 241 ALHAIERCKHYVELLVAOGADVAOARGFPQPKDGGYFYRGEELPLSLAACNQH 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVLAVALADNRENTKFTKXYDILLKCARLPDPS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAVALADNRENTKFTKXYDILLKCARLPDPS 360
Qy 361 NLEAVLNNDGSLPLMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAGPVYSSLYD 420
Db 361 NLEAVLNNDGSLPLMAAKTKIGIFOHIIIRREVTDEDTRLSRKFKOMAGPVYSSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYL 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINEILRDKMRKFGAVSFYINVSYL 480
Qy 481 AMVIFTLTAAVYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Db 481 AMVIFTLTAAVYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTINIKOLFMMKCGV 540
Qy 541 NSLFDGSPOLLFYISVLYVSALYLAGIEAYLAVVFPALVGMNALYFTRGKLTG 600
Db 541 NSLFDGSPOLLFYISVLYVSALYLAGIEAYLAVVFPALVGMNALYFTRGKLTG 600
Qy 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLNPKANKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIOKILFKDLFRFLVYLPMIGYASALVSLNPKANKVCNEDQNTCTVPTPSC 660
Qy 661 RDSEFTSTFLDLFLTLTGMDLEMLSTKYPVVFIILVTYIILFTVLLNMLTALMGE 720
Db 661 RDSEFTSTFLDLFLTLTGMDLEMLSTKYPVVFIILVTYIILFTVLLNMLTALMGE 720
Qy 721 TVGVSKESKHIWKIQ 736
Db 721 TVGVSKESKHIWKIQ 736

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## RESULT 15

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US-10-342-844-60
; Sequence 60, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, Gyn_1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAC28029
; DATABASE ENTRY DATE: 2000-10-31
US-10-342-844-60

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Query Match 85.6%; Score 635; DB 15; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSLANLFGCEDGSLSPSPADASRPAGP 60
Db 1 MADSSGPRAGPGGEVAILPGDESGTPGGEAFPLSLANLFGCEDGSLSPSPADASRPAGP 60

```

```
QY 61 GGRPELAKMKFOGAPRKGVNPIDILESTLYESSVVPGEKAPMDSLFDYGYRRHSSDN 120
|
|
|
Db 61 GGRPELAKMKFOGAPRKGVNPIDILESTLYESSVVPGEKAPMDSLFDYGYRRHSSDN 120
|
|
|
QY 121 KWRKKIIEKQSPKAPAPQPPPIIKVNNRPIIPDIVSRGSTADIDGLPPLTHKKRL 180
|
|
|
Db 121 KWRKKIIEKQSPKAPAPQPPPIIKVNNRPIIPDIVSRGSTADIDGLPPLTHKKRL 180
|
|
|
QY 181 TDEEPEPESTGTCCLPKALINTSNGRNDTIPVLIDIAERTGAMREPTNSPPRDIYYRGOT 240
|
|
|
Db 181 TDEEPEPESTGTCCLPKALINTSNGRNDTIPVLIDIAERTGAMREPTNSPPRDIYYRGOT 240
|
|
|
QY 241 ALHIAIERCKHYVELLVAQADVAHQAGREFQPKDEGYYFGEPLPLSLAQTNOPI 300
|
|
|
Db 241 ALHIAIERCKHYVELLVAQADVAHQAGREFQPKDEGYYFGEPLPLSLAQTNOPI 300
|
|
|
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLLCARLPDS 360
|
|
|
Db 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIADNTRENTKFTYKMYDILLLCARLPDS 360
|
|
|
QY 361 NLEAVLNDGSLPLMAAATGKIGIPQHTIRREVTDETRHLSRKEKOWAYGVPYSSLYD 420
|
|
|
Db 361 NLEAVLNDGSLPLMAAATGKIGIPQHTIRREVTDETRHLSRKEKOWAYGVPYSSLYD 420
|
|
|
QY 421 LSSLDTGCEEASVLEILVYNSKIENHEMLAVEPINELDRKMRKFGAVSYINVSYLQ 480
|
|
|
Db 421 LSSLDTGCEEASVLEILVYNSKIENHEMLAVEPINELDRKMRKFGAVSYINVSYLQ 480
|
|
|
QY 481 AMVIFLTLAYIQPLEGTPPYPTTYDYLRLAGEVITLFTGVLFFTNTKDLFMKCPGV 540
|
|
|
Db 481 AMVIFLTLAYIQPLEGTPPYPTTYDYLRLAGEVITLFTGVLFFTNTKDLFMKCPGV 540
|
|
|
QY 541 NSLFDGSPQLYFYISVIVISAALYLAGIEAYLAVMFEALVGMNALYFTRGKLTG 600
|
|
|
Db 541 NSLFDGSPQLYFYISVIVISAALYLAGIEAYLAVMFEALVGMNALYFTRGKLTG 600
|
|
|
QY 601 TYSIMIÖKILFKDLFRLLVYLLFMIGVASALVSLNPCANMKVCNEQDQNTCTVPTPSC 660
|
|
|
Db 601 TYSIMIÖKILFKDLFRLLVYLLFMIGVASALVSLNPCANMKVCNEQDQNTCTVPTPSC 660
|
|
|
QY 661 RDETFSTFLDLFKLTIGMDLEMLSSTKYPVVFIIILVTYIILFVLLINMLIALMGE 720
|
|
|
Db 661 RDETFSTFLDLFKLTIGMDLEMLSSTKYPVVFIIILVTYIILFVLLINMLIALMGE 720
|
|
|
QY 721 TVGQVSKESKHITKIQ 736
|
|
|
Db 721 TVGQVSKESKHITKIQ 736
|
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Search completed: December 2, 2004, 22:58:10  
Job time : 151 secs